

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Yelton, Dale E.  
Rosok, Mae Joanne

(ii) TITLE OF THE INVENTION: A METHOD FOR INHIBITING IMMUNOGLOBULIN-  
INDUCED TOXICITY RESULTING FROM THE USE OF IMMUNOGLOBULINS IN  
THERAPY AND IN VIVO DIAGNOSIS

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
(B) STREET: 11150 Santa Monica Boulevard, Suite 400  
(C) CITY: Los Angeles  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 90025

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/905,293  
(B) FILING DATE: 01-AUG-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/023,033  
(B) FILING DATE: 02-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Canady, Karen S  
(B) REGISTRATION NUMBER: 39,927  
(C) REFERENCE/DOCKET NUMBER: 30436.43USU1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 310-445-1140  
(B) TELEFAX: 310-445-9031  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGCACCGAA AGCTTTCTGG GGCAGGCCAG GCCTGA

36

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCCGGACATG TTGGTACCCA CGTGGTGGTC GACGCTGAGC CTGGCTTCGA GCAGACA

57

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCGACCACC ACGTGGGTAC CAACATGTCC GGAGCCACAT GGACAGAGGC CGGCT

55

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGGTTCTTG GTCATCTCCT CTCTAGATGG

30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACCATGGTCG ACCTCAGACC TGCCAAGAGC CATATC

36

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cont.

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATGGTCACG TGGTGTGTCC CTGGATGCAG GCTACTCTAG

40

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGGGAGGGA GGGTGTCTGC TGGAAGCCAG GCTCAGCGCT GACCTCAGA

49

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGAAAGAACC ATCACAGTCT CGCAGGGGCC CAGGGCAGCG CTGGGTGCTT

50

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACGGATCGG GAGATCTGCT AGGTGACCTG AGGCGCGCCG GCTTCGAATA GCCAGAGTAA 60  
CCTTTTTTTT TAATTTTATT TTATTTTATT TTTGAGATGG AGTTTGGCGC CGATCTCCCG 120  
ATCCCCTATG GTCGACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAGTATC 180  
TGCTCCCTGC TTTGTGTGTTG GAGGTCGCTG AGTAGTGC GC GAGCAAAATT TAAGCTACAA 240  
CAAGGCAAGG CTTGACCGAC AATTGCATGA AGAATCTGCT TAGGGTTAGG CGTTTTGCGC 300

TGCTTCGCGA	TGTACGGGCC	AGATATACGC	GTTGACATTG	ATTATTGACT	AGTTATTAAT	360
AGTAATCAAT	TACGGGGTCA	TTAGTTTCATA	GCCCATATAT	GGAGTTCCGC	GTTACATAAC	420
TTACGGTAAA	TGGCCCGCCT	GGCTGACCGC	CCAACGACCC	CCGCCCATTG	ACGTCAATAA	480
TGACGTATGT	TCCCATAGTA	ACGCCAATAG	GGACTTTCCA	TTGACGTCAA	TGGGTGGACT	540
ATTTACGGTA	AACTGCCCAC	TTGGCAGTAC	ATCAAGTGTA	TCATATGCCA	AGTACGCCCC	600
CTATTGACGT	CAATGACGGT	AAATGGCCCG	CCTGGCATTG	TGCCCAGTAC	ATGACCTTAT	660
GGGACTTTCC	TACTTGCCAG	TACATCTACG	TATTAGTCAT	CGCTATTACC	ATGGTGATGC	720
GGTTTGGCA	GTACATCAAT	GGGCGTGGAT	AGCGGTTTGA	CTCACGGGGA	TTTCCAAGTC	780
TCCACCCCAT	TGACGTCAAT	GGGAGTTTGT	TTTGGCACCA	AAATCAACGG	GACTTTCCAA	840
AATGTCGTAA	CAACTCCGCC	CCATTGACGC	AAATGGGCGG	TAGGCGTGTA	CGGTGGGAGG	900
TCTATATAAG	CAGAGCTCTC	TGGCTAACTA	GAGAACCCAC	TGCTTACTGG	CTTATCGAAA	960
TTAATACGAC	TCATATAGG	GAGACCCAAG	CTTGGTACCA	ATTTAAATG	ATATCTCCTT	1020
AGGTCTCGAG	TCCTTAGATA	ACCGGTCAAT	CGATTGGAAT	TCTTGCGGCC	GCTTGCTAGC	1080
CACCATGGAG	TTGTGGTTAA	GCTTGGTCCT	TCCTTGTCCT	TGTTTTAAAA	GGTGTCCAGT	1140
GTGAAGTGAA	TCTGGTGGAG	TCTGGGGGAG	GCTTAGTGCA	GCCTGGAGGG	TCCCTGAAAG	1200
TCTCCTGTGT	AACCTCTGGA	TTCACTTTCA	GTGACTATTA	CATGTATTGG	GTTCCGCCAGA	1260
CTCCAGAGAA	GAGGCTGGAG	TGGGTCGCAT	ACATTAGTCA	AGGTGGTGAT	ATAACCGACT	1320
ATCCAGAGAC	GTAAAGGGT	CGATTACCA	TCTCCAGAGA	CAATGCCAAG	AACACCTGT	1380
ACCTGCAAA	GAGCCGTCTG	AAGTCTGAGG	ACACAGCCAT	GTATTACTGT	GCAAGAGGCC	1440
TGGACGACGG	GGCCTGGTTT	GCTTACTGGG	GCCAAGGGAC	TCTGGTCACG	GTCTCTGTAG	1500
CTAGACCAA	GGGCCCATCG	GTCTTCCCCC	TGGCACCCCT	CTCCAAGAGC	ACCTCTGGGG	1560
GCACAGCGGC	CCTGGGCTGC	CTGGTCAAGG	ACTACTTCCC	CGAACCCTGT	ACGGTGTCTG	1620
GGAACTCAGG	CGCCCTGACC	AGCGGCGTGC	ACACCTTCCC	GGCTGTCCCTA	CAGTCCTCAG	1680
GACTCTACTC	CCTCAGCAGC	GTGGTCACCG	TGCCCTCCAG	CAGCTTGGGC	ACCCAGACCT	1740
ACATCTGCAA	CGTGAATCAC	AAGCCCAGCA	ACACCAAGGT	GGACAAGAAA	GTTGGTGAGA	1800
GGCCAGCACA	GGGAGGGAGG	GTGTCTGCTG	GAAGCCAGGC	TCAGCGCTCC	TGCCTGGACG	1860
CATCCCGGCT	ATGCAGCCCC	AGTCCAGGGC	AGCAAGGCAG	GCCCCGTCTG	CCTCTTACC	1920
CGGAGGCCTC	TGCCCGCCCC	ACTCATGCTC	AGGGAGAGGG	TCTTCTGGCT	TTTTCCCCAG	1980
GCTCTGGGCA	GGCACAGGCT	AGGTGCCCCCT	AACCCAGGCC	CTGCACACAA	AGGGGCAGGT	2040
GCTGGGCTCA	GACCTGCCAA	GAGCCATATC	CGGGAGGACC	CTGCCCCCTGA	CCTAAGCCCA	2100
CCCCAAAGGC	CAAACCTCTC	ACTCCCTCAG	CTCGGACACC	TTCTCTCCTC	CCAGATTCCA	2160
GTAACCTCCA	ATCTTCTCTC	TGCAGAGCCC	AAATCTTGTG	ACAAAACCTCA	CACATGCCCA	2220
CCGTGCCCCG	GTAAGCCAGC	CCAGGCCTCG	CCCTCCAGCT	CAAGGCGGGA	CAGGTGCCCT	2280
AGAGTAGCCT	GCATCCAGGG	ACAGGCCCCA	GCCGGGTGCT	GACACGTCCA	CCTCCATCTC	2340
TTCTCTAGCA	CCTGAACCTC	TGGGGGGACC	GTCAGTCTTC	CTCTTCCCCC	CAAAACCCAA	2400
GGACACCTCT	ATGATCTCCC	GGACCCCTGA	GGTCACATGC	GTGGTGGTGG	ACGTGAGCCA	2460
CGAAGACCTT	GAGGTCAAGT	TCAACTGGTA	CGTGGACGGC	GTGGAGGTGC	ATAATGCCAA	2520
GACAAAGCCG	CGGGAGGAGC	AGTACAACAG	CACGTACCGT	GTGGTCAGCG	TCCTCACCGT	2580
CCTGCACCAG	GACTGGCTGA	ATGGCAAGGA	GTACAAGTGC	AAGGTCTCCA	ACAAAGCCCT	2640
CCCAGCCCCC	ATCGAGAAAA	CCATCTCCAA	AGCCAAAGGT	GGGACCCGTG	GGGTGCGAGG	2700
GCCACATGGA	CAGAGGCCGG	CTCGGCCAC	CCTCTGCCCT	GAGAGTGACC	GCTGTACCAA	2760
CCTCTGTCCC	TACAGGGCAG	CCCCGAGAAC	CACAGGTGTA	CACCCTGCCC	CCATCCCGGG	2820
ATGAGCTGAC	CAAGAACCAG	GTCAGCCTGA	CCTGCCTGGT	CAAAGGCTTC	TATCCCAGCG	2880
ACATCGCCGT	GGAGTGGGAG	AGCAATGGGC	AGCCGGAGAA	CAACTACAAG	ACCACGCCCTC	2940
CCGTGCTGGA	CTCCGACGGC	TCCTTCTTCC	TCTACAGCAA	GCTCACCGTG	GACAAGAGCA	3000
GGTGGCAGCA	GGGGAACGTC	TTCTCATGCT	CCGTGATGCA	TGAGGCTCTG	CACAACCACT	3060
ACACGCAGAA	GAGCCTCTCC	CTGTCTCCGG	GTAAATGAGT	GCGACGGCCG	GCAAGCCCCC	3120
GCTCCCCGGG	CTCTCGCGGT	CGCACGAGGA	TGCTTGGCAC	GTACCCCTG	TACATACTTC	3180
CCGGGCGCCC	AGCATGGA	TAAAGCACCC	AGCGCTGCCC	TGGGCCCTG	CGAGACTGTG	3240
ATGGTTCTTT	CCACGGGTCA	GGCCGAGTCT	GAGGCCTGAG	TGGCATGAGG	GAGGCAGAGC	3300
GGGTCCCACT	GTCCCCACAC	TGGCCCAGGC	TGTGCAGGTG	TGCCTGGGCC	CCCTAGGGTG	3360
GGGCTCAGCC	AGGGGCTGCC	CTCGGCAGGG	TGGGGGATTT	GCCAGCGTGG	CCCTCCCTCC	3420
AGCAGCACCT	GCCCTGGGCT	GGGCCACGGG	AAGCCCTAGG	AGCCCTGGG	GACAGACACA	3480
CAGCCCCTGC	CTCTGTAGGA	GACTGTCTTG	TTCTGTGAGC	GCCCCTGTCC	TCCCGACCTC	3540
CATGCCCACT	CGGGGGCATG	CCTAGTCCAT	GTGCGTAGGG	ACAGGCCCTC	CCTCACCCAT	3600
CTACCCCCAC	GGCACTAACC	CCTGGCTGCC	CTGCCAGCC	TCGCACCCCG	ATGGGGACAC	3660
AACCGACTCC	GGGGACATGC	ACTCTCGGGC	CCTGTGGAGG	GACTGGTGCA	GATGCCACACA	3720
CACACACTCA	GCCCAGACCC	GTTCAACAAA	CCCCGCACTG	AGGTGGGCCG	GCCACACGGC	3780
CACCACACAC	ACACGTGCAC	GCCTCACACA	CGGAGCCTCA	CCCGGGCGAA	CTGCACAGCA	3840
CCCAGACCAG	AGCAAGGTCC	TCGCACACGT	GAACACTCCT	CGGACACAGG	CCCCACAGAG	3900

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CCCCACGCGG	CACCTCAAGG	CCCACGAGCC	TCTCGGCAGC	TTCTCCACAT	GCTGACCTGC	3960
TCAGACAAAC	CCAGCCCTCC	TCTCACAAGG	GTGCCCCTGC	AGCCGCCACA	CACACACAGG	4020
GGATCACACA	CCACGTACAG	TCCCTGGCCC	TGGCCCACCT	CCCAGTGCCG	CCCTTCCCTG	4080
CAGGACGGAT	CAGCCTCGAC	TGTGCCTTCT	AGTTGCCAGC	CATCTGTTGT	TTGCCCCTCC	4140
CCCGTGCCTT	CCTTGACCCT	GGAAGGTGCC	ACTCCCACCT	TCCTTTCCTA	ATAAAATGAG	4200
GAAATTGCAT	CGCATTGTCT	GAGTAGGTGT	CATTCTATTC	TGGGGGGTGG	GGTGGGGCAG	4260
GACAGCAAGG	GGGAGGATTG	GGAAGACAAT	AGCAGGCATG	CTGGGGATGC	GGTGGGCTCT	4320
ATGGCTTCTG	AGGCGGAAAG	AACCAGCTGG	GGCTCTAGGG	GGTATCCCCA	CGCGCCCTGT	4380
AGCGGCGCAT	TAAGCGCGGC	GGGTGTGGTG	GTTACGCGCA	GCGTGACCGC	TACACTTGCC	4440
AGCGCCCTAG	CGCCCGCTCC	TTTCGCTTTC	TTCCCTTCCCT	TTCTCGCCAC	GTTCGCGGGG	4500
CCTCTCAAAA	AAGGGAAGAA	AAGCATGCAT	CTCAATTAGT	CAGCAACCAT	AGTCCCGCCC	4560
CTAACTCCGC	CCATCCCGCC	CCTAACTCCG	CCCAGTTCGG	CCCATTCTCC	GCCCCATGGC	4620
TGACTAATTT	TTTTTATTTA	TGCAGAGGCC	GAGGCCGCCT	CGGCCTCTGA	GCTATTCCAG	4680
AAGTAGTGAG	GAGGCTTTTT	TGGAGGCCTA	GGCTTTTGCA	AAAAGCTTGG	ACAGCTCAGG	4740
GCTGCGATTT	CGCGCCAAAC	TTGACGGCAA	TCCTAGCGTG	AAGGCTGGTA	GGATTTTATC	4800
CCCGCTGCCA	TCATGGTTCC	ACCATTGAAC	TGCATCGTCG	CCGTGTCCCA	AAATATGGGG	4860
ATTGGCAAGA	ACGGAGACCT	ACCCTGGCCT	CCGCTCAGGA	ACGAGTTCAA	GTACTTCCAA	4920
AGAATGACCA	CAAGCTCTTC	AGTGGAAAGT	AAACAGAATC	TGGTGATTAT	GGGTAGGAAA	4980
ACCTGGTTCT	CCATTCTCTG	GAAGAATCGA	CCTTTAAAGG	ACAGAATTAA	TATAGTTCTC	5040
AGTAGAGAAC	TCAAAGAACC	ACCACGAGGA	GCTCATTTTC	TTGCCAAAAG	TTTGGATGAT	5100
GCCTTAAGAC	TTATTGAACA	ACCGGAATTG	GCAAGTAAAG	TAGACATGGT	TTGGATAGTC	5160
GGAGGCAGTT	CTGTTTACCA	GGAAGCCATG	AATCAACCAG	GCCACCTTAG	ACTCTTTGTG	5220
ACAAGGATCA	TGCAGGAATT	TGAAAGTGAC	ACGTTTTTCC	CAGAAATTGA	TTTGGGAAAA	5280
TATAAACTTC	TCCCAGAATA	CCCAGGCGTC	CTCTCTGAGG	TCCAGGAGGA	AAAAGGCATC	5340
AAGTATAAGT	TTGAAGTCTA	CGAGAAGAAA	GACTAACAGG	AAGATGCTTT	CAAGTTCTCT	5400
GCTCCCTTCC	TAAAGCTATG	CATTTTTATA	AGACCATGGG	ACTTTTGCTG	GCTTTAGATC	5460
CTTTTGTGAA	GGAACTTAC	TTCTGTGGTG	TGACATAATT	GGACAACTA	CCTACAGAGA	5520
TTTAAAGCTC	TAAAGTAAAT	ATAAAATTTT	TAAGTGTATA	ATGTGTTAAA	CTACTGATTC	5580
TAATTGTTTG	TGTATTTTAG	ATTCCAACCT	ATGGAACCTG	TGAATGGGAG	CAGTGGTGGA	5640
ATGCCTTTAA	TGAGGAAAAC	CTGTTTTGCT	CAGAAGAAAT	GCCATCTAGT	GATGATGAGG	5700
CTACTGCTGA	CTCTCAACAT	TCTACTCCTC	CAAAAAAGAA	GAGAAAGGTA	GAAGACCCCA	5760
AGGACTTTCC	TTTCAAGATT	CTAAGTTTTT	TGAGTCATGC	TGTGTTTAGT	AATAGAACTC	5820
TTGCTTGCTT	TGCTATTTAC	ACCACAAAGG	AAAAAGCTGC	ACTGCTATAC	AAGAAAATTA	5880
TGGAAAAATA	TTCTGTAAAC	TTTATAAGTA	GGCATAACAG	TTATAATCAT	AACATACTGT	5940
TTTTTCTTAC	TCCACACAGG	CATAGAGTGT	CTGCTATTAA	TAACTATGCT	CAAAAATTGT	6000
GTACCTTTAG	CTTTTAAATT	TGTAAAGGGG	TTAATAAGGA	ATATTTGATG	TATAGTGCCT	6060
TGACTACAGA	TCATAATCAG	CCATACCACA	TTTGTAGAGG	TTTTACTTGC	TTTAAAAAAC	6120
CTCCACACAC	TCCCCCTGAA	CCTGAAACAT	AAAATGAATG	CAATTGTTGT	TGTTAACTTG	6180
TTTATTGCAG	CTTATAATGG	TTACAAATAA	AGCAATAGCA	TCACAAATTT	CACAAATAAA	6240
GCATTTTTTT	CACTGCATTG	TAGTTGTGGT	TTGTCCAAAC	TCATCAATGT	ATCTTATCAT	6300
GTCTGGATCG	GCTGGATGAT	CCTCCAGCGC	GGGGATCTCA	TGCTGGAGTT	CTTCGCCCAC	6360
CCCAACTTGT	TTATTGCAGC	TTATAATGGT	TACAAATAAA	GCAATAGCAT	CACAAATTTT	6420
ACAAATAAAG	CATTTTTTTT	ACTGCATTCT	AGTTGTGGTT	TGTCCAAACT	CATCAATGTA	6480
TCTTATCATG	TCTGTATACC	GTCGACCTCT	AGCTAGAGCT	TGGCGTAATC	ATGGTCATAG	6540
CTGTTTCCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	ACAACATACG	AGCCGGAAGC	6600
ATAAAGTGTA	AAGCCTGGGG	TGCCTAATGA	GTGAGCTAAC	TCACATTAAT	TGCGTTGCGC	6660
TCACTGCCCC	CTTCCAGTTC	GGGAAACCTG	TCGTGCCAGC	TGCATTAATG	AATCGGCCAA	6720
CGCGCGGGGA	GAGGCGGTTT	GCGTATTGGG	CGCTCTTCCG	CTTCCTCGCT	CACTGACTCG	6780
CTGCGCTCGG	TCGTTCCGGT	GCGGCGAGCG	GTATCAGCTC	ACTCAAAGGC	GGTAATACGG	6840
TTATCCACAG	AATCAGGGGA	TAACGCAGGA	AAGAACATGT	GAGCAAAAGG	CCAGCAAAAG	6900
GCCAGGAACC	GTAAAAAGGC	CGCGTTGCTG	CGCTTTTTTC	ATAGGCTCCG	CCCCCTGAC	6960
GAGCATCACA	AAAATCGACG	CTCAAGTCAG	AGGTGGCGAA	ACCCGACAGG	ACTATAAAGA	7020
TACCAGGCGT	TTCCCCCTGG	AAGCTCCCTC	GTGCGCTCTC	CTGTTCCGAC	CCTGCCGCTT	7080
ACCGGATACC	TGTCCGCCTT	TCTCCCTTCG	GGAAGCGTGG	CGCTTTCTCA	ATGCTCACGC	7140
TGTAGGTATC	TCAGTTCGGT	GTAGGTCGTT	CGCTCCAAGC	TGGGCTGTGT	GCACGAACCC	7200
CCGTTTACG	CCGACCGCTG	CGCCTTATCC	GGTAACATATC	GTCTTGAGTC	CAACCCGGTA	7260
AGACACGACT	TATCGCCACT	GGCAGCAGCC	ACTGGTAACA	GGATTAGCAG	AGCGAGGTAT	7320
GTAGGCGGTG	CTACAGAGTT	CTTGAAGTGG	TGGCCTAACT	ACGGCTACAC	TAGAAGGACA	7380
GTATTTGGTA	TCTGCGCTCT	GCTGAAGCCA	GTTACCTTCG	GAAAAAGAGT	TGGTAGCTCT	7440
TGATCCGGCA	AACAAACCAC	CGCTGGTAGC	GGTGGTTTTT	TTGTTTGCAA	GCAGCAGATT	7500

ACGCGCAGAA	AAAAAGGATC	TCAAGAAGAT	CCTTTGATCT	TTTCTACGGG	GTCTGACGCT	7560
CAGTGGAACG	AAAACCTCACG	TTAAGGGATT	TTGGTCATGA	GATTATCAAA	AAGGATCTTC	7620
ACCTAGATCC	TTTTAAATTA	AAAATGAAGT	TTTAAATCAA	TCTAAAGTAT	ATATGAGTAA	7680
ACTTGGTCTG	ACAGTTACCA	ATGCTTAATC	AGTGAGGCAC	CTATCTCAGC	GATCTGTCTA	7740
TTTCGTTTCT	CCATAGTTGC	CTGACTCCCC	GTCGTGTAGA	TAACCTACGAT	ACGGGAGGGC	7800
TTACCATCTG	GCCCCAGTGC	TGCAATGATA	CCGCGAGACC	CACGCTCACC	GGCTCCAGAT	7860
TTATCAGCAA	TAAACCAGCC	AGCCGGAAGG	GCCGAGCGCA	GAAGTGGTCC	TGCAACTTTA	7920
TCCGCTCCA	TCCAGTCTAT	TAATTGTTGC	CGGGAAGCTA	GAGTAAGTAG	TTCGCCAGTT	7980
AATAGTTTGC	GCAACGTTGT	TGCCATTGCT	ACAGGCATCG	TGGTGTACAG	CTCGTCGTTT	8040
GGTATGGCTT	CATTTCAGCTC	CGGTTCCCAA	CGATCAAGGC	GAGTTACATG	ATCCCCCATG	8100
TTGTGCAAAA	AAGCGGTTAG	CTCCTTCGGT	CCTCCGATCG	TTGTGAGAAG	TAAGTTGGCC	8160
GCAGTGTTAT	CACTCATGGT	TATGGCAGCA	CTGCATAATT	CTCTTACTGT	CATGCCATCC	8220
GTAAGATGCT	TTTCTGTGAC	TGGTGAGTAC	TCAACCAAGT	CATTCTGAGA	ATAGTGTATG	8280
CGGCGACCGA	GTTGCTCTTG	CCCGGCGTCA	ATACGGGATA	ATACCGCGCC	ACATAGCAGA	8340
ACTTTAAAG	TGCTCATCAT	TGGAAAACGT	TCTTCGGGGC	GAAGACTCTC	AAGGATCTTA	8400
CCGCTGTTGA	GATCCAGTTC	GATGTAACCC	ACTCGTGAC	CCAACTGATC	TTCAGCATCT	8460
TTTACTTTCA	CCAGCGTTTC	TGGGTGAGCA	AAAACAGGAA	GGCAAAATGC	CGCAAAAAAG	8520
GGAAATAAGG	CGACACGGAA	ATGTTGAATA	GCATACACTC	TCCTTTTTC	ATATTATTGA	8580
AGCATTTATC	AGGGTTATTG	TCTCATGAGC	GGATACATAT	TTGAATGTAT	TTAGAAAAAT	8640
AAACAAATAG	GGGTTCCGCG	CACATTTCCC	CGAAAAGTGC	CACCTGACGT	C	8691

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GACGGATCGG	GAGATCTGCT	AGGTGACCTG	AGGCGCGCCG	GCTTCGAATA	GCCAGAGTAA	60
CCTTTTTTTT	TAATTTTATT	TTATTTTATT	TTTGAGATGG	AGTTTGGCGC	CGATCTCCCG	120
ATCCCCTATG	GTCGACTCTC	AGTACAATCT	GCTCTGATGC	CGCATAGTTA	AGCCAGTATC	180
TGCTCCCTGC	TTGTGTGTTG	GAGGTGCTG	AGTAGTGCGC	GAGCAAAATT	TAAGCTACAA	240
CAAGGCAAGG	CTTGACCGAC	AATTGCATGA	AGAATCTGCT	TAGGGTTAGG	CGTTTTGCGC	300
TGCTTCGCGA	TGTACGGGCC	AGATATACGC	GTTGACATTG	ATTATTGACT	AGTTATTAAAT	360
AGTAATCAAT	TACGGGGTCA	TTAGTTTATA	GCCCATATAT	GGAGTTCCGC	GTTACATAAC	420
TTACGGTAAA	TGGCCCGCCT	GGCTGACCGC	CCAACGACCC	CCGCCCATTG	ACGTCAATAA	480
TGACGTATGT	TCCCATAGTA	ACGCCAATAG	GGACTTTCCA	TTGACGTCAA	TGGGTGGACT	540
ATTTACGGTA	AACTGCCCCA	TTGGCAGTAC	ATCAAGTGTA	TCATATGCCA	AGTACGCCCC	600
CTATTGACGT	CAATGACGGT	AAATGGCCCC	CCTGGCATT	TGCCCAGTAC	ATGACCTTAT	660
GGGACTTTCC	TACTTGGCAG	TACATCTACG	TATTAGTCAT	CGCTATTACC	ATGGTGATGC	720
GTTTTTGGCA	GTACATCAAT	GGGCGTGGAT	AGCGGTTTGA	CTCACGGGGA	TTTCCAAGTC	780
TCCACCCCAT	TGACGTCAAT	GGGAGTTTGT	TTTGGCACCA	AAATCAACGG	GACTTTCCAA	840
AATGTCGTAA	CAACTCCGCC	CCATTGACGC	AAATGGGCGG	TAGGCGTGTA	CGGTGGGAGG	900
TCTATATAAG	CAGAGCTCTC	TGGCTAACTA	GAGAACCCAC	TGCTTACTGG	CTTATCGAAA	960
TTAATACGAC	TCACTATAGG	GAGACCCAAG	CTTGGTACCA	ATTTAAATTG	ATATCTCCTT	1020
AGGTCTCGAG	TCTCTAGATA	ACCGGTCAAT	CGATTGGAAT	TCTTGCGGCC	GCTTGCTAGC	1080
CACCATGGAG	TTGTGGTTAA	GCTTGGTCTT	TCCTTGTCCT	TGTTTTAAAA	GGTGTCCAGT	1140
GTGAAGTGAA	TCTGGTGGAG	TCTGGGGGAG	GCTTAGTGCA	GCCTGGAGGG	TCCCTGAAAG	1200
TCTCCTGTGT	AACCTCTGGA	TTCACTTTCA	GTGACTATTA	CATGTATTGG	GTTCCGCCAGA	1260
CTCCAGAGAA	GAGGCTGGAG	TGGGTGCGAT	ACATTAGTCA	AGGTGGTGAT	ATAACCGACT	1320
ATCCAGACAC	TGTAAAGGGT	CGATTACCA	TCTCCAGAGA	CAATGCCAAG	AACACCTGT	1380
ACCTTGCAAT	GAGCCGTCTG	AAGTCTGAGG	ACACAGCCAT	GTATTACTGT	GCAAGAGGCC	1440
TGGACGACGG	GGCCTGGTTT	GCTTACTGGG	GCCAAGGGAC	TCTGGTCACG	GTCTCTGTAG	1500
CTAGCACCAA	GGGCCCATCG	GTCTTCCCCC	TGGCACCCCT	CTCCAAGAGC	ACCTCTGGGG	1560
GCACAGCGGC	CCTGGGCTGC	CTGGTCAAGG	ACTACTTCCC	CGAACCGGTG	ACGGTGTCTG	1620

B'  
wax.

B'   
 104.

GGA	ACT	CAGG	CGCC	TGACC	AGCG	GCGTGC	ACAC	CTTCCC	GGCT	GTCTTA	CAGT	CCTCAG	1680
GACT	CTACTC	CCTCAGCAGC	GTGGTCAACG	TGCCCTCCAG	CAGCTTGGGC	ACCCAGACCT							1740
ACAT	CTGCAA	CGTGAATCAC	AAGCCCAGCA	ACACCAAGGT	GGACAAGAAA	GTTGGTGAGA							1800
GGCC	AGCACA	GGGAGGGAGG	GTGTCTGCTG	GAAGCCAGGC	TCAGCGCTCC	TGCCGTGGACG							1860
CATCCC	GGGCT	ATGCAGCCCC	AGTCCAGGGC	AGCAAGGCAG	GCCCCGTCTG	CCTCTTCACC							1920
CGGAGG	CCTC	TGCCCCCCCC	ACTCATGCTC	AGGGAGAGGG	TCTTCTGGCT	TTTTCCCCAG							1980
GCTCT	TGGGCA	GGCACAGGCT	AGGTGCCCTC	AACCCAGGCC	CTGCACACA	AGGGGCAGGT							2040
CTGTGGG	CTCA	GACCTGCCAA	GAGCCATATC	CGGGAGACC	CTGCCCTGA	CCTAAGCCCA							2100
CCCCAA	AAGGC	CAAACTCTCC	ACTCCCTCAG	CTCGGACACC	TTCTCTCTC	CCAGATTCCA							2160
GTA	ACTCCCA	ATCTTCTCTC	TGCAGAGCCC	AAATCTTGTG	ACAAA	ACTCA	CACATGCCCA						2220
CCGTG	CCCCAG	GTAAGCCAGC	CCAGGCTCG	CCCTCCAGCT	CAAGGCGGGA	CAGGTGCCCT							2280
AGAGT	AGCCT	GCATCCAGGG	ACACACCACG	TGGGTACCAA	CATGTCGGGA	GCCACATGGA							2340
CAGAGG	CCCG	CTCGGCCAC	CCTCTGCCCT	GAGAGTGACC	GCTGTACCAA	CCTCTGTCCC							2400
TACAGGG	CAG	CCCCGAGAAC	CACAGGTGTA	CACCCTGCCC	CCATCCCGGG	ATGAGCTGAC							2460
CAAGA	AACCAG	GTCAGCCTGA	CCTGCCTGGT	CAAAGGCTTC	TATCCCAGCG	ACATCGCCGT							2520
GGAGT	TGGGAG	AGCAATGGGC	AGCCGAGAA	CAACTACAAG	ACCACGCCTC	CCGTGCTGGA							2580
TCCG	ACGGC	TCCTTCTTCC	TCTACAGCAA	GCTCACCGTG	GACAAGAGCA	GGTGCGACGA							2640
GGGGA	ACGTC	TTCTCATGCT	CCGTGATGCA	TGAGGCTCTG	CACAACCACT	ACACGCAGAA							2700
GAGCCT	CTCC	CTGTCTCCGG	GTA	AATGAGT	GCGACGGCCG	GCAAGCCCC	GCTCCCCGGG						2760
CTCTC	GCGGT	CGCACGAGGA	TGCTTGGCAC	GTACCCCCTG	TACATACTTC	CCGGGCGCCC							2820
AGCAT	TGAAA	TAAAGCACCC	AGCGCTGCCC	TGGGCCCCTG	CGAGACTGTG	ATGGTTCTTT							2880
CCACG	GGGTCA	GGCCGAGTCT	GAGGCTGAG	TGGCATGAGG	GAGGCAGAGC	GGGTCCCACT							2940
GTCCCC	ACAC	TGGCCCAGGC	TGTGCAGGTG	TGCCTGGGCC	CCCTAGGGTG	GGGCTCAGCC							3000
AGGGG	CTGCC	CTCGGCAGGG	TGGGGGATTT	GCCAGCGTGG	CCCTCCCTC	AGCAGCACCT							3060
GCCTT	TGGGCT	GGCCACGGG	AAGCCCTAGG	AGCCCCTGGG	GACAGACACA	CAGCCCTGCG							3120
CTCTG	TAGGA	GACTGTCTG	TTCTGTGAGC	GCCCCGTGCC	TCCCGACTC	CATGCCCACT							3180
CGGGG	GCATG	CCTAGTCCAT	GTGCGTAGGG	ACAGGCCCTC	CCTCACCCAT	CTACCCCCAC							3240
GGCACT	AACC	CCTGGCTGCC	CTGCCAGCC	TCGCACCCGC	ATGGGGACAC	AACCGACTCC							3300
GGGGA	CATGC	ACTCTCGGGC	CCTGTGGAGG	GACTGGTGCA	GATGCCACA	CACACTCA							3360
GCCC	AGACCC	GTTCAACAA	CCCCGCACTG	AGGTTGGCCG	GCCACACGGC	CACCACACAC							3420
ACACG	TGCAC	GCCTCACACA	CGGAGCCTCA	CCCGGGCGAA	CTGCACAGCA	CCCAGACCAG							3480
AGCA	AGGTCC	TCGCACACGT	GAACACTCCT	CGGACACAGG	CCCCACGAG	CCCCACGCGG							3540
CACCT	CAAGG	CCCACGAGCC	TCTCGGACG	TTCTCCACAT	GCTGACCTGC	TCAGACAAAC							3600
CCAGC	CCCTCC	TCTCACAAAG	GTGCCCTGCG	AGCCGCCACA	CACACACAGG	GGATCACACA							3660
CCACG	TACAG	TCCTTGCCCC	TGGCCCACTT	CCCAGTGCCG	CCCTTCCCTG	CAGGACGGAT							3720
CAGCCT	TCGAC	TGTGCCTTCT	AGTTGCCAGC	CATCTGTTGT	TTGCCCTCC	CCCGTGCTT							3780
CCTTG	ACCCT	GGAAGGTGCC	ACTCCC	ACTG	TCCTTTCCTA	ATAAAATGAG	GAAATTGCAT						3840
CGCAT	TGTCT	GAGTAGGTGT	CATTCTATT	TGGGGGGTGG	GGTGGGGCAG	GACAGCAAGG							3900
GGGAG	GATTG	GGAAGACAA	AGCAGGCATG	CTGGGGATGC	GGTGGGCTCT	ATGGCTTCTG							3960
AGGCG	GAAAG	AACCAGCTGG	GGCTCTAGGG	GGTATCCCCA	CGCGCCCTGT	AGCGGCGCAT							4020
TAAGC	GCGCGC	GGGTGTGGTG	GTTACGCGCA	GCGTGACCCG	TACACTTGCC	AGCGCCCTAG							4080
CGCCG	CTCC	TTTCGCTTTC	TTCCCTTCT	TTCTCGCCAC	GTTCCGCGGG	CCTCTCAAAA							4140
AAGGG	AAAAA	AAGCATGCAT	CTCA	ATTAGT	CAGCA	AACCAT	AGTCCCCGCC	CTAACTCCGC					4200
CCATC	CCCGC	CCTAACTCCG	CCCAGTTCCG	CCCATTCTCC	GCCCCATGGC	TGACTAATTT							4260
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GAGGCT	TTTTT	TGGAGGCC	GGCTTTTGCA	AAAAGCTTGG	ACAGCTCAGG	GCTGCGATTT							4380
CGCGC	CAAAAC	TTGACGGCAA	TCCTAGCGTG	AAGGCTGGTA	GGATTTTATC	CCCGCTGCCA							4440
TCATG	GGTTG	ACCATTGAAC	TGCATCGTCG	CCGTGTCCCA	AAATATGGGG	ATTGGCAAGA							4500
ACGGAG	ACCT	ACCCTGGCCT	CCGCTCAGGA	ACGAGTTC	GTACTTCCAA	AGAATGACCA							4560
CAACCT	CTTTC	AGTGAAGGT	AAACAGAA	TGTTGATTAT	GGGTAGGAAA	ACCTGGTTCT							4620
CCATT	CCTGA	GAGA	AATCGA	CCTTTAAAGG	ACAGAATTAA	TATAGTTCTC	AGTAGAGAAC						4680
TCAA	AGAACC	ACCACGAGGA	GCTCATTTTC	TTGCCAAAAG	TTTGGATGAT	GCCTTAAGAC							4740
TTATT	GAAACA	ACCGGAATTG	GCAAGTAAAG	TAGACATGGT	TTGGATAGTC	GGAGGCAGTT							4800
CTGTT	TACCA	GGAAGCCATG	AATCAACCAG	GCCACCTTAG	ACTCTTTGTG	ACAAGGATCA							4860
TGCAG	GAAAT	TGAAAGTGAC	ACGTTTTTCC	CAGAAATTGA	TTTGGGGAAA	TATAAACTTC							4920
TCCC	GAAATA	CCCAGGCGTC	CTCTCTGAGG	TCCAGGAGGA	AAAAGGCATC	AAGTATAAGT							4980
TTGA	AGTCTA	CGAGAAGAAA	GACTAACAGG	AAGATGCTTT	CAAGTTCTCT	GCTCCCCCTCC							5040
TAAAG	CTATG	CATTTTTATA	AGACCATGGG	ACTTTTGCTG	GCTTTAGATC	TCTTTGTGAA							5100
GGAAC	CTTAC	TTCTGTGGTG	TGACATAATT	GGACAACTA	CCTACAGAGA	TTTAAAGCTC							5160
TAAGG	TAAAT	ATAAAATTTT	TAAGTGTATA	ATGTGTTAAA	CTACTGATTC	TAATTGTTTG							5220

8' cont.

TGTATTTTAG	ATTCCAACCT	ATGGAACCTGA	TGAATGGGAG	CAGTGGTGGA	ATGCCTTTAA	5280
TGAGGAAAAC	CTGTTTTGCT	CAGAAGAAAT	GCCATCTAGT	GATGATGAGG	CTACTGCTGA	5340
CTCTCAACAT	TCTACTCCTC	CAAAAAAGAA	GAGAAAGGTA	GAAGACCCCA	AGGACTTTCC	5400
TTCAGAATTG	CTAAGTTTTT	TGAGTCATGC	TGTGTTTTAGT	AATAGAACTC	TTGCTTGCTT	5460
TGCTATTTAC	ACCACAAAGG	AAAAAGCTGC	ACTGCTATAC	AAGAAAATTA	TGGAAAAATA	5520
TTCTGTAACC	TTTATAAGTA	GGCATAACAG	TTATAATCAT	AACATACTGT	TTTTTCTTAC	5580
TCCACACAGG	CATAGAGTGT	CTGCTATTAA	TAACATATGCT	CAAAAATTGT	GTACCTTTAG	5640
CTTTTAAATT	TGTAAAGGGG	TTAATAAGGA	ATATTTGATG	TATAGTGCCT	TGACTAGAGA	5700
TCATAATCAG	CCATACCACA	TTTGTAGAGG	TTTTACTTGC	TTTAAAAAAC	CTCCACACC	5760
TCCCCCTGAA	CCTGAAACAT	AAAATGAATG	CAATTGTTGT	TGTTAACTTG	TTTATTGCAG	5820
CTTATAATGG	TTACAAATAA	AGCAATAGCA	TCACAAATTT	CACAAATAAA	GCATTTTTTT	5880
CACTGCATTG	TAGTTGTGGT	TTGTCCAAAC	TCATCAATGT	ATCTTATCAT	GTCTGGATCG	5940
GCTGGATGAT	CCTCCAGCGC	GGGGATCTCA	TGCTGGAGTT	CTTCGCCAC	CCCAACTTGT	6000
TTATTGCAGC	TTATAATGGT	TACAAATAAA	GCAATAGCAT	CACAAATTTC	ACAAATAAAG	6060
CATTTTTTTC	ACTGCATTCT	AGTTGTGGTT	TGTCCAAACT	CATCAATGTA	TCTTATCATG	6120
TCTGTATACC	GTCGACCTCT	AGCTAGAGCT	TGGCGTAATC	ATGGTCATAG	CTGTTTCCTG	6180
TGTGAAATTG	TTATCCGCTC	ACAATTCAC	ACAACATACG	AGCCGGAAGC	ATAAAGTGTA	6240
AAGCCTGGGG	TGCCTAATGA	GTGAGCTAAC	TCACATTAAT	TGCGTTGCCG	TCACTGCCCG	6300
CTTTCCAGTC	GGGAAACCTG	TCGTGCCAGC	TGCATTAATG	AATCGGCCAA	CGCGCGGGGA	6360
GAGGCGGTTT	GCGTATTGGG	CGCTCTTCCG	CTTCTCGCT	CACTGACTCG	CTGCGCTCGG	6420
TCGTTCCGGT	GCGGCGAGCG	GTATCAGCTC	ACTCAAAGGC	GGTAATACGG	TTATCCACAG	6480
AATCAGGGGA	TAACGCAGGA	AAGAACATGT	GAGCAAAAGG	CCAGCAAAAG	GCCAGGAACC	6540
GTAAAAAGGC	CGCGTTGCTG	GCGTTTTTCC	ATAGGCTCCG	CCCCCTGAC	GAGCATCACA	6600
AAAATCGACG	CTCAAGTCAG	AGGTGGCGAA	ACCCGACAGG	ACTATAAAGA	TACCAGGCGT	6660
TTCCCCCTGG	AAGCTCCCTC	GTGCGCTCTC	CTGTTCCGAC	CCTGCCGCTT	ACCGGATACC	6720
TGTCCGCCTT	TCTCCCTTCG	GGAAGCGTGG	CGCTTCTCA	ATGCTCACGC	TGTAGGTATC	6780
TCAGTTCGGT	GTAGGTCGTT	CGCTCCAAGC	TGGGCTGTGT	GCACGAACCC	CCCGTTCAGC	6840
CCGACCGGTG	CGCCTTATCC	GTAACATATC	GTCTTGAGTC	CAACCCGTA	AGACACGACT	6900
TATCGCCACT	GGCAGCAGCC	ACTGGTAACA	GGATTAGCAG	AGCGAGGTAT	GTAGGCGGTG	6960
CTACAGAGTT	CTTGAAGTGG	TGGCCTAACT	ACGGCTACAC	TAGAAGGACA	GTATTTGGTA	7020
TCTGCGCTCT	GCTGAAGCCA	GTTACCTTCG	GAAAAAGAGT	TGGTAGCTCT	TGATCCGGCA	7080
AACAAACCAC	CGCTGGTAGC	GGTGGTTTTT	TTGTTTGCAA	GCAGCAGATT	ACGCGCAGAA	7140
AAAAAGGATC	TCAAGAAGAT	CCTTTGATCT	TTTCTACGGG	GTCTGACGCT	CAGTGGAAACG	7200
AAAATCAGC	TTAAGGGATT	TTGGTCATGA	GATTATCAAA	AAGGATCTTC	ACCTAGATCC	7260
TTTTAAATTA	AAAATGAAGT	TTTAAATCAA	TCTAAAGTAT	ATATGAGTAA	ACTTGGTCTG	7320
ACAGTTACCA	ATGCTTAATC	AGTGAGGCAC	CTATCTCAGC	GATCTGTCTA	TTTCGTTTCT	7380
CCATAGTTGC	CTGACTCCCC	GTGCTGTAGA	TAACATACGAT	ACGGGAGGGC	TTACCATCTG	7440
GCCCCAGTGC	TGCAATGATA	CCGCGAGACC	CACGCTCACC	GGCTCCAGAT	TTATCAGCAA	7500
TAAACCAGCC	AGCCGGAAGG	GCCGAGCGCA	GAAGTGGTCC	TGCAACTTTA	TCCGCCTCCA	7560
TCCAGTCTAT	TAATTGTTGC	CGGGAAGCTA	GAGTAAGTAG	TTCGCCAGTT	AATAGTTTGC	7620
GCAACGTTGT	TGCCATTGCT	ACAGGCATCG	TGGTGTACAG	CTCGTCGTTT	GGTATGGCTT	7680
CATTGAGCTC	CGGTTCCCAA	CGATCAAGGC	GAGTTACATG	ATCCCCCATG	TTGTGCAAAA	7740
AAGCGGTTAG	CTCCTTCGGT	CCTCCGATCG	TTGTGAGAAG	TAAGTTGGCC	GCAGTGTAT	7800
CACTCATGGT	TATGGCAGCA	CTGCATAATT	CTCTTACTGT	CATGCCATCC	GTAAGATGCT	7860
TTTCTGTGAC	TGGTGAGTAC	TCAACCAAGT	CATTCTGAGA	ATAGTGTATG	CGGCGACCGA	7920
GTTGCTCTTG	CCCGGCGTCA	ATACGGGATA	ATACCGCGCC	ACATAGCAGA	ACTTTAAAAG	7980
TGTCATCAT	TGGAAAAACGT	TCTTCGGGGC	GAAAACTCTC	AAGGATCTTA	CCGCTGTTGA	8040
GATCCAGTTC	GATGTAACCC	ACTCGTGCAC	CCAACTGATC	TTCAGCATCT	TTTACTTTCA	8100
CCAGCGTTTC	TGGGTGAGCA	AAAACAGGAA	GGCAAAATGC	CGCAAAAAAG	GGAATAAGGG	8160
CGACACGGAA	ATGTTGAATA	CTCATACTCT	TCCTTTTTCA	ATATTATTGA	AGCATTTATC	8220
AGGGTTATTG	TCTCATGAGC	GGATACATAT	TTGAATGTAT	TTAGAAAAAT	AAACAAATAG	8280
GGGTTCCGCG	CACATTTCCC	CGAAAAGTGC	CACCTGACGT	C		8321

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGCAC CATGAAGTTG CCTGTTAGGC 60  
TGTTGGTGCT GATGTTCTGG ATTCTGCTT CCAGCAGTGA TGTTTTGATG ACCCAAATTC 120  
CAGTCTCCCT GCCTGTCAGT CTGGGAGATC AAGCGTCCAT CTCTGCAGA TCTAGTCAGA 180  
TCATTGTACA TAATAATGGC AACACCTATT TAGAATGGTA CCTGCAGAAA CCAGGCCAGT 240  
CTCCACAGCT CCTGATCTAC AAAGTTTCCA ACCGATTTTC TGGGGTCCCA GACAGGTTCA 300  
GCGGCAGTGG ATCAGGGACA GATTTACAC TCAAGATCAG CAGAGTGGAG GCTGAGGATC 360  
TGGGAGTTTA TTACTGCTTT CAAGGTTTCA ATGTTCCATT CACGTTCCGC TCGGGGACAA 420  
AGTTGGAAT AAAACGTAAG TCTCGAGTCT CTAGATAACC GGTCAATCGA TTGGAATTCT 480  
AAACTCTGAG GGGGTGCGAT GACGTGGCCA TTCTTTGCCT AAAGCATTGA GTTTACTGCA 540  
AGGTCAGAAA AGCATGCAAA GCCCTCAGAA TGGCTGCAAA GAGCTCCAAC AAAACAATTT 600  
AGAACTTTAT TAAGGAATAG GGGGAAGCTA GGAAGAACT CAAAACATCA AGATTTTAAA 660  
TACGTTCTTT GGTCTCCTTG CTATAATTAT CTGGGATAAG CATGCTGTTT TCTGTCTGTC 720  
CCTAACATGC CCTATCCGC AAACAACACA CCCAAGGGCA GAACTTTGT ACTTAAACAC 780  
CATCTGTTT GCTTCTTTCC TCAGGAACTG TGGCTGCACC ATCTGTCTTC ATCTTCCCGC 840  
CATCTGATGA GCAGTTGAAA TCTGGAAGT CCTCTGTTGT GTGCCTGCTG AATAACTTCT 900  
ATCCACAGAGA GGCCAAAGTA CAGTGAAGG TGGATAACGC CCTCCAATCG GGTAACCTCC 960  
AGGAGAGTGT CACAGAGCAG GAGAGCAAG ACAGCACCTA CAGCCTCAGC AGCACCTGA 1020  
CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG 1080  
GCCTGAGCTC GCCCGTCACA AAGAGCTTCA ACAGGGGAGA GTGTTAGAGG GAGAAGTGCC 1140  
CCCACCTGCT CCTCAGTTCC AGCCTGACCC CCTCCCATCC TTTGGCCTCT GACCCTTTT 1200  
CCACAGGGGA CCTACCCCTA TTGCGGTCTT CCAGCTCATC TTTCACCTCA CCCCCCTCCT 1260  
CCTCCTTGGC TTTAATTATG CTAATGTTGG AGGAGAATGA ATAAATAAAG TGAATCTTTG 1320  
CACCTGTGGT TTCTCTCTTT CCTCATTTAA TAATTATTAT CTGTTGTTT ACCAACTACT 1380  
CAATTTCTCT TATAAGGGAC TAAATATGTA GTCATCCTAA GGCACGTAAC CATTTATAAA 1440  
AATCATCCTT CATTTCTATT TACCCTATCA TCCTCTGCAA GACAGTCTC CCTCAAACCC 1500  
ACAAGCCTTC TGCTCTACA GTCCCTGGG CCATGGTAGG AGAGACTTGC TTCCTTGTTC 1560  
TCCCTCCTC AGCAAGCCCT CATAGTCCTT TTTAAGGGTG ACAGGTCTTA CAGTCATATA 1620  
TCCTTTGATT CAATTCCTG AGAATCAACC AAAGCAAATT TTTCAAAAGA AGAAACCTGC 1680  
TATAAAGAGA ATCATTCAAT GCAACATGAT ATAAAATAAC AACACAATAA AAGCAATTAA 1740  
ATAAACAAAC AATAGGGAAA TGTTTAAGTT CATCATGGTA CTTAGACTTA ATGGAATGTC 1800  
ATGCCCTATT TACATTTTAA AACAGGTACT GAGGGACTCC TGTCTGCCAA GGGCCGTATT 1860  
GAGTACTTTC CACAACCTAA TTTAATCCAC ACTATACTGT GAGATTAAAA ACATTCAATTA 1920  
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ACTTCTAGAT GACTGAGTGT CCCCACCCAC CAAAAAATA TGCAAGAATG TTCAAAGCAG 2040  
CTTTATTTAC AAAAGCCAAA AATTGGAAAT AGCCCGATTG TCCAACAATA GAATGAGTTA 2100  
TTAACTGTG GTATGTTTAT ACATTAGAAT ACCCAATGAG GAGAATTAAAC AAGCTACAAC 2160  
TATACCTACT CACACAGATG AATCTCATAA AAATAATGTT ACATAAGAGA AACTCAATGC 2220  
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TCTTATACCC AGTTAATAGA TAGAAGAGGA ATAAGTAATA GGTCAAGACC AACGCAGCTG 2520  
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TGGGAAGGA CAGTCAATGA GAAACTACAT AAGGAAGCAC CTGCCCCTT TGCCTCTTGA 3060  
GAATGTTGAT GAGTATCAAA TCTTTCAAAC TTTGGAGGTT TGAGTAGGGG TGAGACTCAG 3120  
TAATGTCCCT TCCAATGACA TGAACCTGCT CACTCATCCC TGGGGGCCAA ATTGAACAAT 3180  
CAAAGGCAGG CATAATCCAG TTATGAATTC TTGCGGCCGC TTGCTAGCTT CACGTGTTGG 3240  
ATCCAACCGC GGAAGGGCCC TATCTATAG TGTCACCTAA ATGCTAGAGC TCGCTGATCA 3300

8'  
cont.

GCCTCGACTG	TGCCTTCTAG	TTGCCAGCCA	TCTGTTGTTT	GCCCCCCCC	CGTGCCTTCC	3360
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CATTGTCTGA	GTAGGTGTCA	TTCTATTCTG	GGGGGTGGGG	TGGGGCAGGA	CAGCAAGGGG	3480
GAGGATTGGG	AAGACAATAG	CAGGCATGCT	GGGGATGCGG	TGGGCTCTAT	GGCTTCTGAG	3540
GCGGAAAGAA	CCAGCTGGGG	CTCTAGGGGG	TATCCCCACG	CGCCCTGTAG	CGGCGCATTA	3600
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CCCGCTCCTT	TCGCTTTCTT	CCCTTCCTTT	CTCGCCACGT	TCGCCGGGCC	TCTCAAAAAA	3720
GGGAAAAAAA	GCATGCATCT	CAATTAGTCA	GCAACCATAG	TCCCGCCCCT	AACTCCGCCC	3780
ATCCCGCCCC	TAACTCCGCC	CAGTTCCGCC	CATTCTCCGC	CCCATGGCTG	ACTAATTTT	3840
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GGCTTTTTTG	GAGGCCTAGG	CTTTTGCAAA	AAGCTTGGAC	AGCTCAGGGC	TGCGATTTTC	3960
CGCCAAACTT	GACGGCAATC	CTAGCGTGAA	GGCTGGTAGG	ATTTTATCCC	CGCTGCCATC	4020
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ATTCTTGAGA	AGAATCGACC	TTTAAAGGAC	AGAATTAATA	TAGTTCCTAG	TAGAGAACTC	4260
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CAGGAATTTG	AAAGTGACAC	GTTTTTCCCA	GAAATTGATT	TGGGGAAATA	TAAACTTCTC	4500
CCAGAATACC	CAGGCGTCTT	CTCTGAGGTC	CAGGAGGAAA	AAGGCATCAA	GTATAAGTTT	4560
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AACCTTACTT	CTGTGGTGTG	ACATAATTGG	ACAAACTACC	TACAGAGATT	TAAAGCTCTA	4740
AGGTAAATAT	AAAATTTTTA	AGTGTATAAT	GTGTTAAACT	ACTGATTCTA	ATTGTTTTGTG	4800
TATTTTAGAT	TCCAACCTAT	GGAAGTATG	AATGGGAGCA	GTGGTGGAAT	GCCTTTAATG	4860
AGGAAAACCT	GTTTGTCTCA	GAAGAAATGC	CATCTAGTGA	TGATGAGGCT	ACTGCTGACT	4920
CTCAACATT	TACTCCTCCA	AAAAAGAAGA	GAAAGGTAGA	AGACCCCAAG	GACTTTCCCTT	4980
CAGAATTGCT	AAGTTTTTTG	AGTCATGCTG	TGTTTTAGTAA	TAGAACTCTT	GCTTGCTTTG	5040
CTATTTACAC	CACAAAGGAA	AAAGCTGCAC	TGCTATACAA	GAAAATTATG	GAAAAATATT	5100
CTGTAACCTT	TATAAGTAGG	CATAACAGTT	ATAATCATAA	CATACTGTTT	TTTCTTACTC	5160
CACACAGGCA	TAGAGTGTCT	GCTATTAATA	ACTATGCTCA	AAAATTGTGT	ACCTTTAGCT	5220
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ATAATCAGCC	ATACCACATT	TGTAGAGGTT	TTACTTGCTT	TAAAAAACCT	CCCACACCTC	5340
CCCCTGAACC	TGAAACATAA	AATGAATGCA	ATTGTTGTTG	TAACTTGTTT	TATTGCAGCT	5400
TATAATGGTT	ACAAATAAAG	CAATAGCATC	ACAAATTTCA	CAAATAAAGC	ATTTTTTTTCA	5460
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TGGATGATCC	TCCAGCGCGG	GGATCTCATG	CTGGAGTTCT	TCGCCCCACC	CAACTTGTCT	5580
ATTGCAGCTT	ATAATGGTTA	CAAATAAAGC	AATAGCATCA	CAAATTTTCA	AAATAAAGCA	5640
TTTTTTTTCAC	TGCATTCTAG	TTGTGGTTTG	TCCAAACTCA	TCAATGTATC	TTATCATGTC	5700
TGTATACCGT	CGACCTCTAG	CTAGAGCTTG	GCGTAATCAT	GGTCATAGCT	GTTTCCTGTG	5760
TGAAATTGTT	ATCCGCTCAC	AATTCCACAC	AACATACGAG	CCGGAAGCAT	AAAGTGTAAG	5820
GCCTGGGGTG	CCTAATGAGT	GAGCTAACTC	ACATTAATTG	CGTTGCGCTC	ACTGCCCGCT	5880
TTCCAGTCGG	GAAACCTGTC	GTGCCAGCTG	CATTAATGAA	TCGGCCAACG	CGCGGGGAGA	5940
GGCGGTTTGC	GTATTGGGCG	CTCTTCCGCT	TCCTCGCTCA	CTGACTCGCT	GCGCTCGGTC	6000
GTTCCGCTGC	GGCGAGCGGT	ATCAGCTCAC	TCAAAGGCGG	TAATACGGTT	ATCCACAGAA	6060
TCAGGGGATA	ACGCAGGAAA	GAACATGTGA	GCAAAAGGCC	AGCAAAAGGC	CAGGAACCGT	6120
AAAAAGGCCG	CGTTGCTGGC	GTTTTTCCAT	AGGCTCCGCC	CCCCTGACGA	GCATCACAAA	6180
AATCGACGCT	CAAGTCAGAG	GTGGCGAAAC	CCGACAGGAC	TATAAAGATA	CCAGGCGTTT	6240
CCCCCTGGAA	GCTCCCTCGT	GCGCTCTCCT	GTTCCGACCC	TGCCGCTTAC	CGGATACCTG	6300
TCCGCTTTTC	TCCCTTCGGG	AAGCGTGGCG	CTTCTCAAT	GCTCACGCTG	TAGGTATCTC	6360
AGTTCCGGTG	AGTTCGTTTC	CTCCAAGCTG	GGCTGTGTGC	ACGAACCCCC	CGTTCAGCCC	6420
GACCGCTGCG	CCTTATCCGG	TAACTATCGT	CTTGAGTCCA	ACCCGGTAAG	ACACGACTTA	6480
TCGCCACTGG	CAGCAGCCAC	TGGTAACAGG	ATTAGCAGAG	CGAGGTATGT	AGGCGGTGCT	6540
ACAGAGTTCT	TGAAGTGGTG	GCCTAACTAC	GGCTACACTA	GAAGGACAGT	ATTTGGTATC	6600
TGCGCTCTGC	TGAAGCCAGT	TACCTTCGGA	AAAAGAGTTG	GTAGCTCTTG	ATCCGGCAAA	6660
CAAACCATCG	CTGGTAGCGG	TGGTTTTTTT	TTTTTGCAAGC	AGCAGATTAC	GCGCAGAAAA	6720
AAAGGATCTC	AAGAAGATCC	TTTGATCTTT	TCTACGGGGT	CTGACGCTCA	GTGGAACGAA	6780
AACTCACGTT	AAGGGATTTT	GGTCATGAGA	TTATCAAAAA	GGATCTTCAC	CTAGATCCTT	6840
TTAAATTAAA	AATGAAGTTT	TAAATCAATC	TAAAGTATAT	ATGAGTAAAC	TTGGTCTGAC	6900

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AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTCATCC 6960  
 ATAGTTGCCT GACTCCCCGT CGTGTAAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC 7020  
 CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACC GG CTCCAGATTT ATCAGCAATA 7080  
 AACCAAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC CGCCTCCATC 7140  
 CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGCGC 7200  
 AACGTTGTTG CCATTGCTAC AGGCATCGTG GTGTACCGCT CGTCGTTTGG TATGGCTTCA 7260  
 TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA 7320  
 GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTTATCA 7380  
 CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT 7440  
 TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCGAGT 7500  
 TGCTCTTGCC CGGCGTCAAT ACGGGATAAT ACCGCGCCAC ATAGCAGAAC TTTAAAAGTG 7560  
 CTCATCATTG GAAAACGTTT TTCGGGGCGA AAACCTCTCA GGATCTTACC GCTGTTGAGA 7620  
 TCCAGTTCGA TGTAAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTTACC 7680  
 AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG AATAAGGGCG 7740  
 ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTATATCAG 7800  
 GGTATTGTG TCATGAGCGG ATACATATTT GAATGTATTT AGAAAAATAA ACAAAATAGGG 7860  
 GTTCCGCGCA CATTTCCTCCG AAAAGTGCCA CCTGACGTCG ACGGATCGGG AGATCTGCTA 7920  
 GCCCGGGTGA CCTGAGGCGC GCCGGCTTCG AATAGCCAGA GTAACTTTT TTTTAAATTT 7980  
 TATTTTATTT TATTTTGGAG ATGGAGTTTG GCGCCGATCT CCCGATCCCC TATGGTCGAC 8040  
 TCTCAGTACA ATCTGCTCTG ATGCCGCATA GTTAAGCCAG TATCTGCTCC CTGCTTGTGT 8100  
 GTTGGAGGTC GCTGAGTAGT GCGCGAGCAA AATTTAAGCT ACAACAAGGC AAGGCTTGAC 8160  
 CGACAATTGC ATGAAGAATC TGCTTAGGGT TAGGCGTTTT GCGCTGCTTC GCGATGTACG 8220  
 GGCCAGATAT ACGCGTTGAC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG 8280  
 GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC 8340  
 GCCTGGCTGA CCGCCCAACG ACCCCCGCCC ATTGACGTCATAAATGACGT ATGTTCCCAT 8400  
 AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GACTATTTAC GGTAAACTGC 8460  
 CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGTACG CCCCCTATTG ACGTCAATGA 8520  
 CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT TTCCTACTTG 8580  
 GCAGTACATC TACGTATTAG TCATCGCTAT TCCATGGTG ATGCGGTTT GGCAGTACAT 8640  
 CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC CCATTGACGT 8700  
 CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAATGTC GTAACAACTC 8760  
 CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA TAAGCAGAGC 8820  
 TCTCTGGCTA ACTAGAGAAC CCACTGCTTA CTGGCTTATC GAAATTAATA CGACTCACTA 8880  
 TAGGGAGACC CAAGCTT 8897

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC GGTCAATCGA 60  
 TTGGAATTCT TGCGGCCGCT TGCTAGCCAC CATGGAGTTG TGGTTAAGCT TGGTCTTCCT 120  
 TGTCCTTGTT TTTAAAGGTG TCCAGTGTGA AGTGCAACTG GTGGAGTCTG GGGGAGGCTT 180  
 AGTGCAGCCT GGAGGGTCCC TGCGACTTTC CTGTGCTGCA TCTGGATTCC CGTTCAGTGA 240  
 CTATTACATG TATTGGGTTT GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT 300  
 TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT TCACCATCTC 360  
 CAGAGACAAT GCAAAGAACA GCCTGTACCT GCAAATGAAC AGCCTGAGGG ACGAGGACAC 420  
 AGCCGTGTAT TACTGTGCAA GAGGCCTGGC GGACGGGGCC TGGTTTGCTT ACTGGGGCCA 480  
 AGGGAATCTG GTCACGGTCT CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC 540  
 ACCCTCCTCC AAGAGCACCT CTGGGGCCCT AGCGGCCCTG GGCTGCGCTG TCAAGGACTA 600  
 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC 660  
 CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TCACCGTGCC 720  
 CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC 780

CAAGGTGGAC	AAGAAAGTTG	GTGAGAGGCC	AGCACAGGGA	GGGAGGGTGT	CTGCTGGAAG	840
CCAGGCTCAG	CGTCTCTGCC	TGGACGCATC	CCGGCTATGC	AGCCCCAGTC	CAGGGCAGCA	900
AGGCAGGCCC	CGTCTGCCTC	TTCAACCCGA	GGCCTCTGCC	CGCCCCACTC	ATGCTCAGGG	960
AGAGGGTCTT	CTGGCTTTTT	CCCCAGGCTC	TGGGCAGGCA	CAGGCTAGGT	GCCCCTAACC	1020
CAGGCCCTGC	ACACAAAGGG	GCAGGTGCTG	GGCTCAGACC	TGCCAAGAGC	CATATCCGGG	1080
AGGACCCTGC	CCCTGACCTA	AGCCCACCCC	AAAGGCCAAA	CTCTCCACTC	CCTCAGCTCG	1140
GACACCTTCT	CTCCTCCCAG	ATTCCAGTAA	CTCCCAATCT	TCTCTCTGCA	GAGCCCAAAT	1200
CTTGTGACAA	AACCTACACA	TGCCCCACGT	GCCCCAGTAA	GCCAGCCCAG	GCCTCGCCCT	1260
CCAGCTCAAG	GCGGGACAGG	TGCCCTAGAG	TAGCCTGCAT	CCAGGGACAC	ACCACGTGGG	1320
TACCAACATG	TCCGGAGCCA	CATGGACAGA	GGCCGGCTCG	GCCCACCCTC	TGCCCTGAGA	1380
GTGACCGCTG	TACCAACCTC	TGTCCCTACA	GGGCAGCCCC	GAGAACCACA	GGTGTACACC	1440
CTGCCCCCAT	CCCGGGATGA	GCTGACCAAG	AACCAGGTCA	GCCTGACCTG	CCTGGTCAAA	1500
GGCTTCTATC	CCAGCGACAT	CGCCGTGGAG	TGGGAGAGCA	ATGGGCAGCC	GGAGAACAAAC	1560
TACAAGACCA	CGCCTCCCGT	GCTGGACTCC	GACGGCTCCT	TCTTCCTCTA	CAGCAAGCTC	1620
ACCGTGGACA	AGAGCAGGTG	GCAGCAGGGG	AACGTCTTCT	CATGCTCCGT	GATGCATGAG	1680
GCTCTGCACA	ACCACTACAC	GCAGAAGAGC	CTCTCCCTGT	CTCCGGGTAA	ATGAGTGCGA	1740
CGGCCGCAAA	GCCCCGCTC	CCCGGGCTCT	CGCGGTCGCA	CGAGGATGCT	TGGCACGTAC	1800
CCCTGTGACA	TACTTCCCGG	GCGCCCAGCA	TGGAAATAAA	GCACCCAGCG	CTGCCCTGGG	1860
CCCCTGCGAG	ACTGTGATGG	TTCTTTCCAC	GGGTGAGGCC	GAGTCTGAGG	CCTGAGTGGC	1920
ATGAGGGAGG	CAGAGCGGGT	CCCCTGTGCC	CCACACTGGC	CCAGGCTGTG	CAGGTGTGCC	1980
TGGGCCCCCT	AGGGTGGGGC	TCAGCCAGGG	GCTGCCCTCG	GCAGGGTGGG	GGATTTGCCA	2040
GCGTGGCCCT	CCCTCCAGCA	GCACCTGCCC	TGGGCTGGGC	CACGGGAAGC	CCTAGGAGCC	2100
CCTGGGGACA	GACACACAGC	CCCTGCCTCT	GTAGGAGACT	GTCCTGTTCT	GTGAGCGCCC	2160
CTGTCCCTCC	GACCTCCATG	CCCACTCGGG	GGCATGCCTA	GTCCATGTGC	GTAGGGACAG	2220
GCCCTCCCTC	ACCCATCTAC	CCCCACGGCA	CTAACCCCTG	GCTGCCCTGC	CCAGCCTCGC	2280
ACCCGCATGG	GGACACAACC	GACTCCGGGG	ACATGCACCT	TCGGGCCCTG	TGGAGGGACT	2340
GGTGCGAGTG	CCACACACAC	CACCTAGCCC	AGACCCGTTT	AACAAACCCC	GCCTGAGGT	2400
TGGCCGGCCA	CACGGCCACC	ACACACACAC	GTGCACGCCT	CACACACGGA	GCCTCACCCG	2460
GGCGAACTGC	ACAGCACCCA	GACCAGAGCA	AGGTCTCTCG	ACACGTGAAC	ACTCCTCGGA	2520
CACAGGCCCC	CACGAGCCCC	ACGCGGCACC	TCAAGGCCCA	CGAGCCTCTC	GGCAGCTTCT	2580
CCACATGCTG	ACCTGCTCAG	ACAAACCCAG	CCCTCCTCTC	ACAAGGGTGC	CCCTGCAGCC	2640
GCCACACACA	CACAGGGGAT	CACACACCAC	GTCACGTCCC	TGGCCCTGGC	CCACTTCCCA	2700
GTGCCGCCCT	TCCTTGACAG	ACGGATCAGC	CTCGACTGTG	CCTTCTAGTT	GCCAGCCATC	2760
TGTTGTTTGC	CCCTCCCCCG	TGCCTTCCTT	GACCCTGGAA	GGTGCCACTC	CCACTGTCTT	2820
TTCTTAATAA	AATGAGGAAA	TTGCATCGCA	TTGTCTGAGT	AGGTGTCAAT	CTATTCTGGG	2880
GGTGGGGGTG	GGGCAGGACA	GCAAGGGGGA	GGATTGGGAA	GACAATAGCA	GGCATGCTGG	2940
GGATGCGGTG	GGCTCTATGG	CTTCTGAGGC	GGAAAGAACC	AGCTGGGGCT	CTAGGGGGTA	3000
TCCCCACGCG	CCCTGTAGCG	GCGCATTAAG	CGCGGCGGGT	GTGGTGGTTA	CGCGCAGCGT	3060
GACCGCTACA	CTTGCCAGCG	CCCTAGCGCC	CGCTCCTTTC	GCTTTCTTCC	CTTCCTTTCT	3120
CGCCACGTTT	GCCGGGCCTC	TCAAAAAAGG	GAAAAAAGC	ATGCATCTCA	ATTAGTCAGC	3180
AACCATAGTC	CCGCCCCCTA	CTCCGCCCAT	CCCGCCCCTA	ACTCCGCCCA	GTTCCGCCCA	3240
TTCTCCGCCC	CATGGCTGAC	TAATTTTTTT	TATTTATGCA	GAGGCCGAGG	CCGCCTCGGC	3300
CTCTGAGCTA	TTCAGAAAGT	AGTGAGGAGG	CTTTTTTGGA	GGCCTAGGCT	TTTGCAAAAA	3360
GCTTGGACAG	CTCAGGGCTG	CGATTTTCGG	CCAAACTTGA	CGGCAATCCT	AGCGTGAAGG	3420
CTGGTAGGAT	TTTATCCCCG	CTGCCATCAT	GGTTCGACCA	TTGAACTGCA	TCGTCGCCGT	3480
GTCCCAAAAT	ATGGGGATTG	GCAAGAACGG	AGACCTACCC	TGGCCTCCGC	TCAGGAACGA	3540
GTTCAAGTAC	TTCCAAAGAA	TGACCACAAC	CTCTTCAGTG	GAAGGTAAAC	AGAATCTGGT	3600
GATTATGGGT	AGGAAAACCT	GGTTCTCCAT	TCCTGAGAAG	AATCGACCTT	TAAAGGACAG	3660
AATTAATATA	GTTCTCAGTA	GAGAACTCAA	AGAACCACCA	CGAGGAGCTC	ATTTTCTTGC	3720
CAAAAGTTTG	GATGATGCCT	TAAGACTTAT	TGAACAACCG	GAATTGGCAA	GTAAAGTAGA	3780
CATGGTTTGG	ATAGTCGGAG	GCAGTTCTGT	TTACCAGGAA	GCCATGAATC	AACCAGGCCA	3840
CCTTAGACTC	TTTGTGACAA	GGATCATGCA	GGAATTTGAA	AGTGACACGT	TTTTCCCAGA	3900
AATTGATTTG	GGGAAATATA	AACTTCTCCC	AGAATACCCA	GGCGTCCTCT	CTGAGGTCCA	3960
GGAGGAAAAA	GGCATCAAGT	ATAAGTTTGA	AGTCTACGAG	AAGAAAGACT	AACAGGAAGA	4020
TGCTTCTCAAG	TTCTCTGCTC	CCCTCCTAAA	GCTATGCATT	TTTATAAGAC	CATGGGACTT	4080
TTGCTGGCTT	TAGATCTCTT	TGTGAAGGAA	CCTTACTTCT	GTGGTGTGAC	ATAATTGGAC	4140
AAACTACCTA	CAGAGATTTA	AAGCTCTAAG	GTAAATATAA	AATTTTTTAAG	TGTATAATGT	4200
GTTAAACTAC	TGATTCTAAT	TGTTTGTGTA	TTTTAGATTC	CAACCTATGG	AACTGATGAA	4260
TGGGAGCAGT	GGTGAATGTC	CTTTAATGAG	GAAAACCTGT	TTTGCTCAGA	AGAAATGCCA	4320
TCTAGTGATG	ATGAGGCTAC	TGCTGACTCT	CAACATTCTA	CTCCTCCAAA	AAAGAAGAGA	4380

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AAGGTAGAAG	ACCCCAAGGA	CTTTCCTTCA	GAATTGCTAA	GTTTTTTGAG	TCATGCTGTG	4440
TTTAGTAATA	GAACTCTTGC	TTGCTTTGCT	ATTTACACCA	CAAAGGAAAA	AGCTGCACTG	4500
CTATACAAGA	AAATTATGGA	AAAATATTCT	GTAACCTTTA	TAAGTAGGCA	TAACAGTTAT	4560
AATCATAACA	TACTGTTTTT	TCTTACTCCA	CACAGGCATA	GAGTGTCTGC	TATTAATAAC	4620
TATGCTCAAA	AATTGTGTAC	CTTTAGCTTT	TTAATTTGTA	AAGGGGTTAA	TAAGGAATAT	4680
TTGATGTATA	GTGCCTTGAC	TAGAGATCAT	AATCAGCCAT	ACCACATTG	TAGAGGTTTT	4740
ACTTGCTTTA	AAAAACCTCC	CACACCTCCC	CCTGAACCTG	AAACATAAAA	TGAATGCAAT	4800
TGTTGTTGTT	AAC TTGTTTA	TTGCAGCTTA	TAATGGTTAC	AAATAAAGCA	ATAGCATCAC	4860
AAATTTTACA	AATAAAGCAT	TTTTTTTCACT	GCATTCTAGT	TGTGGTTTGT	CCAAACTCAT	4920
CAATGTATCT	TATCATGTCT	GGATCGGCTG	GATGATCCTC	CAGCGCGGGG	ATCTCATGCT	4980
GGAGTTCTTC	GCCCAACCCA	ACTTGTTTAT	TGCAGCTTAT	AATGGTTACA	AATAAAGCAA	5040
TAGCATCACA	AATTTACAAA	ATAAAGCATT	TTTTTCACTG	CATTCTAGTT	GTGGTTTGTC	5100
CAAAC TCATC	AATGTATCTT	ATCATGTCTG	TATACCGTCG	ACCTCTAGCT	AGAGCTTGGC	5160
GTAATCATGG	TCATAGCTGT	TTCTGTGTGT	AAATTGTTAT	CCGCTCACAA	TTCCACACAA	5220
CATACGAGCC	GGAAGCATAA	AGTGTAAGC	CTGGGGTGCC	TAATGAGTGA	GCTAACTCAC	5280
ATTAATTGCG	TTGCGCTCAC	TGCCCGCTTT	CCAGTCGGGA	AACCTGTCGT	GCCAGCTGCA	5340
TTAATGAATT	GGCCAACGCG	CGGGGAGAGG	CGGTTGCGT	ATTGGGCGCT	CTTCCGCTTC	5400
CTCGCTCACT	GACTCGCTGC	GCTCGGTCGT	TGCGCTGCGG	CGAGCGGTAT	CAGCTCACTC	5460
AAAGGCGGTA	ATACGGTTAT	CCACAGAATC	AGGGGATAAC	GCAGGAAAGA	ACATGTGAGC	5520
AAAAGGCCAG	CAAAAGGCCA	GGAACCGTAA	AAAGGCCGCG	TTGCTGGCGT	TTTTCCATAG	5580
GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA	TCGACGCTCA	AGTCAGAGGT	GGCGAAACCC	5640
GACAGGACTA	TAAAGATACC	AGGCGTTTCC	CCCTGGAAGC	TCCCTCGTGC	GCTCTCCTGT	5700
TCCGACCCTG	CCGTTTACCG	GATACCTGTC	CGCCTTTCTC	CCTTCGGGAA	GCGTGCGGCT	5760
TTCTCAATGC	TCACGCTGTA	GGTATCTCAG	TTGCGGTGTAG	GTCGTTCCGT	CCAAGCTGGG	5820
CTGTGTGCAC	GAACCCCCCG	TTTACGCCCC	CCGCTGCGCC	TTATCCGGTA	ACTATCGTCT	5880
TGAGTCCAAC	CCGGTAAGAC	ACGACTTATC	GCCACTGGCA	GCAGCCACTG	GTAACAGGAT	5940
TAGCAGAGCG	AGGTATGTAG	GCGGTGCTAC	AGAGTTCTTG	AAGTGGTGGC	CTAACTACGG	6000
CTACACTAGA	AGGACAGTAT	TTGGTATCTG	CGCTCTGCTG	AAGCCAGTTA	CCTTCGGAAA	6060
AAGAGTTGGT	AGCTCTTGAT	CCGGCAAACA	AACCACCGCT	GGTAGCGGTG	GTTTTTTTGT	6120
TTGCAAGCAG	CAGATTACGC	GCAGAAAAAA	AGGATCTCAA	GAAGATCCTT	TGATCTTTTC	6180
TACGGGGTCT	GACGCTCAGT	GGAACGAAAA	CTCACGTTAA	GGGATTTTGG	TCATGAGATT	6240
ATCAAAAAGG	ATCTTCACCT	AGATCCTTTT	AAATTAATAA	TGAAGTTTTA	AATCAATCTA	6300
AAGTATATAT	GAGTAAACTT	GGTCTGACAG	TTACCAATGC	TTAATCAGTG	AGGCACCTAT	6360
CTCAGCGATC	TGTCTATTTT	GTTTCATCCAT	AGTTGCCTGA	CTCCCCGTCG	TGTAGATAAC	6420
TACGATACGG	GAGGGCTTAC	CATCTGGCCC	CAGTGCTGCA	ATGATACCGC	GAGACCCACG	6480
CTCACCGGCT	CCAGATTTAT	CAGCAATAAA	CCAGCCAGCC	GGAAGGGCCG	AGCGCAGAAG	6540
TGGTCCTGCA	ACTTTATCCG	CCTCCATCCA	GTCTATTAAT	TGTTGCCGGG	AAGCTAGAGT	6600
AAGTAGTTTC	CCAGTTAATA	GTTTGCGCAA	CGTTGTTGCC	ATTGCTACAG	GCATCGTGGT	6660
GTCACGCTCG	TCGTTTGGTA	TGGCTTCATT	CAGCTCCGGT	TCCCAACGAT	CAAGGCGAGT	6720
TACATGATCC	CCCATGTTGT	GCAAAAAAGC	GGTTAGCTCC	TTGCGTCTCT	CGATCGTTGT	6780
CAGAAGTAAG	TTGGCCGCAG	TGTTATCACT	CATGGTTATG	GCAGCACTGC	ATAATTCTCT	6840
TACTGTTCATG	CCATCCGTAA	GATGCTTTTC	TGTGACTGGT	GAGTACTCAA	CCAAGTCATT	6900
CTGAGAATAG	TGTATGCGGC	GACCGAGTTG	CTCTTGCCCC	GCGTCAATAC	GGGATAATAC	6960
CGCGCCACAT	AGCAGAACTT	TAAAAGTGCT	CATCATTTGA	AAACGTTCTT	CGGGGCGAAA	7020
ACTCTCAAGG	ATCTTACCGC	TGTTGAGATC	CAGTTCGATG	TAACCCACTC	GTGCACCCAA	7080
CTGATCTTCA	GCATCTTTTA	CTTTCACCAG	CGTTTCTGGG	TGAGCAAAAA	CAGGAAGGCA	7140
AAATGCCGCA	AAAAAGGGAA	TAAGGGCGAC	ACGGAAATGT	TGAATACTCA	TACTCTTCCT	7200
TTTTCAATAT	TATTGAAGCA	TTTATCAGGG	TTATTGTCTC	ATGAGCGGAT	ACATATTTGA	7260
ATGTATTTAG	AAAAATAAAC	AAATAGGGGT	TCCGCGCACA	TTTCCCCGAA	AAGTGCCACC	7320
TGACGTGCGAC	GGATCGGGAG	ATCTGCTAGG	TGACCTGAGG	CGCGCCGGCT	TCGAATAGCC	7380
AGAGTAACCT	TTTTTTTTTAA	TTTTATTTTA	TTTTATTTTT	GAGATGGAGT	TTGGCGCCGA	7440
TCTCCCGATC	CCCTATGGTC	GA CTCTCAGT	ACAATCTGCT	CTGATGCCGC	ATAGTTAAGC	7500
CAGTATCTGC	TCCTTGCTTG	TGTGTTGGAG	GTCGCTGAGT	AGTGCGCGAG	CAAAATTTAA	7560
GCTACAACAA	GGCAAGGCTT	GACCGACAAT	TGCATGAAGA	ATCTGCTTAG	GGTTAGGCGT	7620
TTTGCGCTGC	TTGCGGATGT	ACGGGCCAGA	TATACGCGTT	GACATTGATT	ATTGACTAGT	7680
TATTAATAGT	AATCAATTAC	GGGGTCATTA	GTTTCATAGC	CATATATGGA	GTTCCGCGTT	7740
ACATAACTTA	CGGTAAATGG	CCCGCCTGGC	TGACCGCCCA	ACGACCCCGG	CCCATTGACG	7800
TCAATAATGA	CGTATGTTCC	CATAGTAACG	CCAATAGGGA	CTTTCCATTG	ACGTCAATGG	7860
GTGGACTATT	TACGGTAAAC	TGCCCACTTG	GCAGTACATC	AAGTGTATCA	TATGCCAAGT	7920
ACGCCCCCTA	TTGACGTCAA	TGACGGTAAA	TGGCCCGCCT	GGCATTATGC	CCAGTACATG	7980

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ACCTTATGGG	ACTTTCCTAC	TTGGCAGTAC	ATCTACGTAT	TAGTCATCGC	TATTACCATG	8040
GTGATGCGGT	TTTGGCAGTA	CATCAATGGG	CGTGGATAGC	GGTTTGACTC	ACGGGGATT	8100
CCAAGTCTCC	ACCCCATTTGA	CGTCAATGGG	AGTTTGTTTT	GGCACCAAAA	TCAACGGGAC	8160
TTTCCAAAAT	GTCGTAACAA	CTCCGCCCCA	TTGACGCAAA	TGGGCGGTAG	GCGTGTACGG	8220
TGGGAGGTCT	ATATAAGCAG	AGCTCTCTGG	CTAACTAGAG	AACCCACTGC	TTACTGGCTT	8280
ATCGAAATTA	ATACGACTCA	CTATAGGGAG	ACCCAAGCTT	G		8321

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACGGATCGG	GAGATCTGCT	AGCCCGGGTG	ACCTGAGGCG	CGCCGGCTTC	GAATAGCCAG	60
AGTAACCTTT	TTTTTTAATT	TTATTTTATT	TTATTTTGA	GATGGAGTTT	GGCGCCGATC	120
TCCGATCCC	CTATGGTCGA	CTCTCAGTAC	AATCTGCTCT	GATGCCGCAT	AGTTAAGCCA	180
GTATCTGCTC	CCTGCTTGCT	TGTTGGAGGT	CGCTGAGTAG	TGCGCGAGCA	AAATTTAAGC	240
TACAACAAGG	CAAGGCTTGA	CCGACAATTG	CATGAAGAAT	CTGCTTAGGG	TTAGGCGTTT	300
TGCGCTGCTT	CGCGATGTAC	GGGCCAGATA	TACGCGTTGA	CATTGATTAT	TGACTAGTTA	360
TTAATAGTAA	TCAATTACGG	GGTCATTAGT	TCATAGCCCA	TATATGGAGT	TCCGCGTTAC	420
ATAACTTACG	GTAAATGGCC	CGCCTGGCTG	ACCGCCCAAC	GACCCCGGCC	CATTGACGTC	480
AATAATGACG	TATGTTCCCA	TAGTAACGCC	AATAGGGACT	TTCCATTGAC	GTCAATGGGT	540
GGACTATTTA	CGGTAAACTG	CCCACTTGGC	AGTACATCAA	GTGTATCATA	TGCCAAGTAC	600
GCCCCCTATT	GACGTCAATG	ACGGTAAATG	GCCCGCCTGG	CATTATGCCC	AGTACATGAC	660
CTTATGGGAC	TTTCTACTT	GGCAGTACAT	CTACGTATTA	GTCATCGCTA	TTACCATGGT	720
GATGCGGTTT	TGGCAGTACA	TCAATGGGCG	TGGATAGCGG	TTTGACTCAC	GGGGATTTC	780
AAGTCTCCAC	CCCATTGACG	TCAATGGGAG	TTTGTTTTGG	CACCAAAATC	AACGGGACTT	840
TCCAAAATGT	CGTAACAAC	CCGCCCCATT	GACGCAAATG	GGCGGTAGGC	GTGTACGGTG	900
GGAGGTCTAT	ATAAGCAGAG	CTCTCTGGCT	AACTAGAGAA	CCCACTGCTT	ACTGGCTTAT	960
CGAAATTAAT	ACGACTCACT	ATAGGGAGAC	CCAAGCTTGG	TACCAATTTA	AATTGATATC	1020
TCCTTAGGTC	TCGAGCACCA	TGAAGTTGCC	TGTTAGGCTG	TTGGTGCTGA	TGTTCTGGAT	1080
TCCTGCTTCC	AGCAGTGATG	TTGTCATGAC	CCAAACCCCA	CTGTCCAGTC	CTGTACGCT	1140
TGGACAACCT	GCGTCCATCT	CTTGACATC	TAGTCAGATC	ATTGTACATA	ATAATGGCAA	1200
CACCTATCTG	GAATGGTACC	AGCAGAGACC	AGGGCAGTCT	CCACGGCTCC	TGATCTACAA	1260
AGTTTCCAAC	CGATTTTCTG	GGGTCCCAGA	CAGGTTTCTG	GGCAGTGGAG	CTGGGACAGA	1320
TTTCACACTC	AAGATCAGCA	GAGTGGAGGC	TGAGGATGTG	GGAGTTTACT	ACTGCTTCCA	1380
GGGTTTACAT	GTTCATTCA	CGTTCCGCCA	AGGGACAAAG	TTGGAATCA	AACGTAAGTC	1440
TCGAGTCTCT	AGATAACCGG	TCAATCGATT	GGAATTCTAA	ACTCTGAGGG	GGTCGGATGA	1500
CGTGGCCATT	CTTTGCCTAA	AGCATTGAGT	TTACTGCAAG	GTCAGAAAAG	CATGCAAAGC	1560
CCTCAGAATG	GCTGCAAAGA	GCTCCAACAA	AACAATTTAG	AACTTTATTA	AGGAATAGGG	1620
GGAAGCTAGG	AAGAAACTCA	AAACATCAAG	ATTTTAAATA	CGCTTCTTGG	TCTCCTTGCT	1680
ATAATTATCT	GGGATAAGCA	TGCTGTTTTT	TGTCTGTCCC	TAACATGCCC	TTATCCGCAA	1740
ACAACACACC	CAAGGGCAGA	ACTTTGTTAC	TTAAACACCA	TCCTGTTTGC	TTCTTTCTCT	1800
AGGAACTGTG	GCTGCACCAT	CTGTCTTCAT	CTTCCCGCCA	TCTGATGAGC	AGTTGAAATC	1860
TGGAAGTGGC	TCTGTTGTGT	GCCTGCTGAA	TAATTCTTAT	CCCAGAGAGG	CCAAAGTACA	1920
GTGGAAGGTG	GATAACGCCC	TCCAATCGGG	TAACTCCAG	GAGAGTGTCA	CAGAGCAGGA	1980
GAGCAAGGAC	AGCACCTACA	GCCTCAGCAG	CACCCTGACG	CTGAGCAAAG	CAGACTACGA	2040
GAAACACAAA	GTCTACGCCT	GCGAAGTCAC	CCATCAGGGC	CTGAGCTCGC	CCGTACACAAA	2100
GAGCTTCAAC	AGGGGAGAGT	GTTAGAGGGA	GAAGTGCCCC	CACCTGCTCC	TCAGTTCCAG	2160
CCTGACCCCC	TCCATCCTT	TGGCCTCTGA	CCCTTTTTC	ACAGGGGACC	TACCCCTATT	2220
GCGTCTCTCC	AGCTCATCTT	TCACCTCACC	CCCCTCCTCC	TCCTTGGCTT	TAATTATGCT	2280
AATGTTGGAG	GAGAATGAAT	AAATAAAGTG	AATCTTTGCA	CCTGTGGTTT	CTCTCTTTCC	2340
TCATTTAATA	ATTATTATCT	GTTGTTTTAC	CAACTACTCA	ATTTCTCTTA	TAAGGGACTA	2400
AATATGTAGT	CATCCTAAGG	CACGTAACCA	TTTATAAAAA	TCATCCTTCA	TTCTATTTTA	2460

B' cat.

CCCTATCATC	CTCTGCAAGA	CAGTCCTCCC	TCAAACCCAC	AAGCCTTCTG	TCCTCACAGT	2520
CCCCTGGGCC	ATGGTAGGAG	AGACTTGCTT	CCTTGTTTTT	CCCTCCTCAG	CAAGCCCTCA	2580
TAGTCCTTTT	TAAGGGTGAC	AGGTCTTACA	GTCATATATC	CTTTGATTCA	ATTCCCTGAG	2640
AATCAACCAA	AGCAAATTTT	TCAAAAGAAG	AAACCTGCTA	TAAAGAGAAT	CATTTCATTGC	2700
AACATGATAT	AAAATAACAA	CACAATAAAA	GCAATTAAAT	AAACAAACAA	TAGGGAAATG	2760
TTTAAGTTCA	TCATGGTACT	TAGACTTAAT	GGAATGTCAT	GCCTTATTTA	CATTTTAAAA	2820
CAGGTACTGA	GGGACTCCTG	TCTGCCAAGG	GCCGTATTGA	GTACTTTCCA	CAACCTAATT	2880
TAATCCACAC	TATACTGTGA	GATTAATAAC	ATTCATTAAA	ATGTTGCAAA	GGTTCATATA	2940
AGCTGAGAGA	CAAATATATT	CTATAACTCA	GCAATCCAC	TTCTAGATGA	CTGAGTGTCC	3000
CCACCCACCA	AAAAACTATG	CAAGAATGTT	CAAAGCAGCT	TTATTTACAA	AAGCCAAAAA	3060
TTGGAATAG	CCCGATTGTC	CAACAATAGA	ATGAGTTATT	AAACTGTGGT	ATGTTTATAC	3120
ATTAGAATAC	CCAATGAGGA	GAATTAACAA	GCTACAACCTA	TACCTACTCA	CACAGATGAA	3180
TCTCATAAAA	ATAATGTTAC	ATAAGAGAAA	CTCAATGCAA	AAGATATGTT	CTGTATGTTT	3240
TCATCCATAT	AAAGTTCAAA	ACCAGGTAAA	AATAAAGTTA	GAAATTTGGA	TGGAAATTAC	3300
TCTTAGCTGG	GGGTGGGCGA	GTTAGTGCCT	GGGAGAAGAC	AAGAAGGGGC	TTCTGGGGTC	3360
TTGGTAATGT	TCTGTTCCCT	GTGTGGGGTT	GTGCAGTTAT	GATCTGTGCA	CTGTTCTGTA	3420
TACACATTAT	GCTTCAAAAT	AACCTCACAT	AAAGAACATC	TTATACCCAG	TTAATAGATA	3480
GAAGAGGAAT	AAGTAATAGG	TCAAGACCAA	CGCAGCTGGT	AAGTGGGGGC	CTGGGATCAA	3540
ATAGCTACCT	GCCTAATCCT	GCCCWCTTGA	GCCCTGAATG	AGTCTGCCTT	CCAGGGCTCA	3600
AGGTGCTCAA	CAAAACAACA	GGCCTGCTAT	TTTCCTGGCA	TCTGTGCCCT	GTTTGGCTAG	3660
CTAGGAGCAC	ACATACATAG	AAATTAAATG	AAACAGACCT	TCAGCAAGGG	GACAGAGGAC	3720
AGAATTAACC	TTGCCAGAC	ACTGGAACCC	CATGTATGAA	CACTCACATG	TTTGGGAAGG	3780
GGGAAGGGCA	CATGTAAATG	AGGACTCTTC	CTCATTCTAT	GGGGCACTCT	GGCCCTGCCC	3840
CTCTCAGCTA	CTCATCCATC	CAACACACCT	TTCTAAGTAC	CTCTCTCTGC	CTACACTCTG	3900
AAGGGGTTCA	GGAGTAACTA	ACACAGCATC	CCTTCCCTCA	AATGACTGAC	AATCCCTTTG	3960
TCCTGCTTTG	TTTTTCTTTT	CAGTCAGTAC	TGGGAAAGTG	GGGAAGGACA	GTATGGAGA	4020
AACTACATAA	GGAAGCACCT	TGCCCTTCTG	CCTCTTGAGA	ATGTTGATGA	GTATCAAAATC	4080
TTTCAAACCT	TGGAGGTTTG	AGTAGGGTGG	AGACTCAGTA	ATGTCCCTTC	CAATGACATG	4140
AACTTGCTCA	CTCATCCCTG	GGGGCCAAAT	TGAACAATCA	AAGGCAGGCA	TAATCCAGTT	4200
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GCCAGCCATC	TGTTGTTTGC	CCCTCCCCCG	TGCCTTCCTT	GACCCTGGAA	GGTGCCACTC	4380
CCACTGTCTT	TTCCTAATAA	AATGAGGAAA	TTGCATCGCA	TTGTCTGAGT	AGGTGTCAAT	4440
CTATTCTGGG	GGGTGGGGTG	GGGCAGGACA	GCAAGGGGGA	GGATTGGGAA	GACAATAGCA	4500
GGCATGCTGG	GGATGCGGTG	GGCTCTATGG	CTTCTGAGGC	GGAAAGAACC	AGCTGGGGCT	4560
CTAGGGGGTG	TCCCCACGCG	CCCTGTAGCG	GCGCATTAAG	CGCGGCGGGT	GTGGTGTTTA	4620
CGCGCAGCGT	GACCGCTACA	CTTGCCAGCG	CCCTAGCGCC	CGCTCCTTTC	GCTTTCTTCC	4680
CCTCCTTTCT	CGCCACGTTT	GCCGGGCCTC	TCAAAAAAAG	GAAAAAAAGC	ATGCATCTCA	4740
ATTAGTCAGC	AACCATAGTC	CCGCCCCCTA	CTCCGCCCCA	CCCGCCCCCTA	ACTCCGCCCCA	4800
GTTCCGCCCC	TTCTCCGCCC	CATGGCTGAC	TAATTTTTTT	TATTTATGCA	GAGGCCGAGG	4860
CCGCTCGGC	CTCTGAGCTA	TTCCAGAAGT	AGTGAGGAGG	CTTTTTTGA	GGCCTAGGCT	4920
TTTGCAAAAA	GCTTGGACAG	CTCAGGGCTG	CGATTTTCGG	CCAAACTTGA	CGGCAATCCT	4980
AGCGTGAAGG	CTGGTAGGAT	TTTATCCCCG	CTGCCATCAT	GGTTCGACCA	TTGAACTGCA	5040
TCGTGCGCGT	GTCCCAAAAT	ATGGGGATTG	GCAAGAACGG	AGACCTACCC	TGGCCTCCGC	5100
TCAGGAACGA	GTTCAAGTAC	TTCCAAAGAA	TGACCACAAC	CTCTTCAGTG	GAAGGTAAAC	5160
AGAACTGTGT	GATTATGGGT	AGGAAAACCT	GGTTCTCCAT	TCCTGAGAAG	AATCGACCTT	5220
TAAAGGACAG	AATTAATATA	GTTCTCAGTA	GAGAACTCAA	AGAACCACCA	CGAGGAGCTC	5280
ATTTTCTTGC	CAAAAGTTTG	GATGATGCCT	TAAGACTTAT	TGAACAACCG	GAATTGGCAA	5340
GTAAAGTAGA	CATGGTTTGG	ATAGTCGGAG	GCAGTTCTGT	TTACCAGGAA	GCCATGAATC	5400
AACCAGGCCA	CCTTAGACTC	TTTGTGACAA	GGATCATGCA	GGAATTTGAA	AGTGACACGT	5460
TTTTCCAGAA	AATTGATTTG	GGGAAATATA	AACTTCTCCC	AGAATACCCA	GGCGTCTCTT	5520
CTGAGGTCCA	GGAGGAAAAA	GGCATCAAGT	ATAAGTTTGA	AGTCTACGAG	AAGAAAGACT	5580
AACAGGAAGA	TGCTTTCAAG	TTCTCTGCTC	CCCTCCTAAA	GCTATGCATT	TTTATAAGAC	5640
CATGGGACTT	TTGCTGGCTT	TAGATCTCTT	TGTGAAGGAA	CCTTACTTCT	GTGGTGTGAC	5700
ATAATTGGAC	AAACTACCTA	CAGAGATTTA	AAGCTCTAAG	GTAAATATAA	AATTTTTAAG	5760
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AACTGATGAA	TGGGAGCAGT	GGTGGAAATG	CTTTAATGAG	GAAAACCTGT	TTTGCTCAGA	5880
AGAAATGCCA	TCTAGTGATG	ATGAGGCTAC	TGCTGACTCT	CAACATTCTA	CTCCTCCAAA	5940
AAAGAAGAGA	AAGGTAGAAG	ACCCCAAGGA	CTTTCCTTCA	GAATTGCTAA	GTTTTTTGAG	6000
TCATGCTGTG	TTTAGTAATA	GAACCTTTGC	TTGCTTTGCT	ATTTACACCA	CAAAGGAAAA	6060

B'  
long

B' cont.

AGCTGCACTG	CTATACAAGA	AAATTATGGA	AAAATATTCT	GTAACCTTTA	TAAGTAGGCA	6120
TAACAGTTAT	AATCATAACA	TACTGTTTTT	TCTTACTCCA	CACAGGCATA	GAGTGTCTGC	6180
TATTAATAAC	TATGCTCAAA	AATTGTGTAC	CTTTAGCTTT	TTAATTTGTA	AAGGGGTTAA	6240
TAAGGAATAT	TTGATGTATA	GTGCCCTTGAC	TAGAGATCAT	AATCAGCCAT	ACCACATTG	6300
TAGAGGTTTT	ACTTGCTTTA	AAAAACCTCC	CACACCTCCC	CCTGAACCTG	AAACATAAAA	6360
TGAATGCAAT	TGTTGTTGTT	AACTTGTTTA	TTGCAGCTTA	TAATGGTTAC	AAATAAAGCA	6420
ATAGCATCAC	AAATTTACACA	AATAAAGCAT	TTTTTTTCACT	GCATTCTAGT	TGTGGTTTGT	6480
CCAAACTCAT	CAATGTATCT	TATCATGTCT	GGATCGGCTG	GATGATCCTC	CAGCGCGGGG	6540
ATCTCATGCT	GGAGTTCTTC	GCCCAACCCA	ACTTGTTTAT	TGCAGCTTAT	AATGGTTACA	6600
AATAAAGCAA	TAGCATCACA	AATTTACAAA	ATAAAGCATT	TTTTTCACTG	CATTCTAGTT	6660
GTGGTTTGTC	CAAACTCATC	AATGTATCTT	ATCATGTCTG	TATACCGTCG	ACCTCTAGCT	6720
AGAGCTTGCG	GTAATCATGG	TCATAGCTGT	TCCTGTGTG	AAATTGTTAT	CCGCTCACAA	6780
TTCCACACAA	CATACGAGCC	GGAAGCATAA	AGTGTAAGC	CTGGGGTGCC	TAATGAGTGA	6840
GCTAACTCAC	ATTAATTGCG	TTGCGCTCAC	TGCCCGCTTT	CCAGTCGGGA	AACCTGTCGT	6900
GCCAGCTGCA	TTAATGAATC	GGCCAACGCG	CGGGGAGAGG	CGGTTTGCGT	ATTGGGCGCT	6960
CTTCCGCTTC	CTCGCTCACT	GACTCGCTGC	GCTCGGTCGT	TCGGCTGCGG	CGAGCGGTAT	7020
CAGCTCACTC	AAAGGCGGTA	ATACGGTTAT	CCACAGAATC	AGGGGATAAC	GCAGGAAAGA	7080
ACATGTGAGC	AAAAGGCCAG	CAAAAGGCCA	GGAAACGTAA	AAAGGCCGCG	TTGCTGGCGT	7140
TTTTCCATAG	GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA	TCGACGCTCA	AGTCAGAGGT	7200
GGCGAAACCC	GACAGGACTA	TAAAGATACC	AGGCGTTTCC	CCCTGGAAGC	TCCCTCGTGC	7260
GCTCTCCTGT	TCCGACCCTG	CCGCTTACCG	GATACCTGTC	CGCCTTTCTC	CCTTCGGGAA	7320
GCGTGGCGCT	TTCTCAATGC	TCACGCTGTA	GGTATCTCAG	TTCGGTGTAG	GTCGTTCTGT	7380
CCAAGCTGGG	CTGTGTGCAC	GAACCCCCCG	TTACGCCCCG	CCGCTGCGCC	TTATCCGCTA	7440
ACTATCGTCT	TGAGTCCAAC	CCGGTAAGAC	ACGACTTATC	GCCACTGGCA	GCAGCCACTG	7500
GTAACAGGAT	TAGCAGAGCG	AGGTATGTAG	GCGGTGCTAC	AGAGTTCTTG	AAGTGGTGGC	7560
CTAACTACGG	CTACACTAGA	AGGACAGTAT	TTGGTATCTG	CGCTCTGCTG	AAGCCAGTTA	7620
CCTTCGGAAA	AAGAGTTGGT	AGCTCTTGAT	CCGGCAAACA	AACCACCGCT	GGTAGCGGTG	7680
GTTTTTTTGT	TTGCAAGCAG	CAGATTACGC	GCAGAAAAAA	AGGATCTCAA	GAAGATCCTT	7740
TGATCTTTTC	TACGGGGTCT	GACGCTCAGT	GGAACGAAAA	CTCACGTTAA	GGGATTTTGG	7800
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AATCAATCTA	AAGTATATAT	GAGTAAACTT	GGTCTGACAG	TTACCAATGC	TTAATCAGTG	7920
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GAGACCCACG	CTCACCGGCT	CCAGATTTAT	CAGCAATAAA	CCAGCCAGCC	GGAAGGGCCG	8100
AGCGCAGAAG	TGGTCCTGCA	ACTTTATCCG	CCTCCATCCA	GTCTATTAAAT	TGTTGCCGGG	8160
AAGCTAGAGT	AAGTAGTTTC	CCAGTTAATA	GTTTGCGCAA	CGTTGTTGCC	ATTGCTACAG	8220
GCATCGTGGT	GTACAGCTCG	TCGTTTGGTA	TGGCTTCATT	CAGCTCCGGT	TCCCAACGAT	8280
CAAGGCGAGT	TACATGATCC	CCCATGTTGT	GCAAAAAAGC	GGTTAGCTCC	TTCGGTCCTC	8340
CGATCGTTGT	CAGAAGTAAG	TTGGCCGCAG	TGTTATCACT	CATGGTTATG	GCAGCACTGC	8400
ATAATTCTCT	TACTGTCTAT	CCATCCGTAA	GATGCTTTTC	TGTGACTGGT	GAGTACTCAA	8460
CCAAGTCATT	CTGAGAATAG	TGTATGCGGC	GACCGAGTTG	CTCTTGCCCC	GCGTCAATAC	8520
GGGATAATAC	CGCGCCACAT	AGCAGAACTT	TAAAAGTGCT	CATCATTGGA	AAACGTTCTT	8580
CGGGGCGAAA	ACTCTCAAGG	ATCTTACCGC	TGTTGAGATC	CAGTTCGATG	TAACCCACTC	8640
GTGCACCCAA	CTGATCTTCA	GCATCTTTTA	CTTTCACCAG	CGTTTCTGGG	TGAGCAAAAA	8700
CAGGAAGGCA	AAATGCCGCA	AAAAAGGGAA	TAAGGGCGAC	ACGGAAATGT	TGAATACTCA	8760
TACTCTTCCT	TTTTCAATAT	TATTGAAGCA	TTTATCAGGG	TTATTGTCTC	ATGAGCGGAT	8820
ACATATTTGA	ATGTATTTAG	AAAAATAAAC	AAATAGGGGT	TCCGCGCACA	TTTCCCCGAA	8880
AAGTGCCACC	TGACGTC					8897

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:



GAAGAGGAAG ACTGACGGTG CCCCCGCGAG TTCAGGTGCT GAGG

44

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCAGCACC TGAAC TCGCG GGGGCACCGT CAGTCTTCCT CTTC

44

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGGGAGGGC TTTGTTGGAG ACCGAGCACG AGTACGACTT GCCATT CAGC C

51

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATGGTTTTTC TCGATGGCGG CTGGGAGGGC

30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCCCTCCAG CCGCCATCGA GAAAACCATC

30

(2) INFORMATION FOR SEQ ID NO:19:

B  
cont.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGTTTTCTCGATAGCGGCTGGGAGGGCTTTG

34

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GATGGTTTTCTCGATGGCGGCTGGGAGGGCTTTGTTGGAGACCGAGCACAGTACGACTTGCCATTCAGCAGTCCTGGTG

60  
81

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CACCAGGACTGGCTGAATGGCAAGTCGTACTCGTGCTCGGTCTCCAACAAAGCCCTCCCAGCCGCCATCGAGAAAACCATC

60  
81

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC GGTCAATCGA  
TTGGAATTCT TCGGCGCGCT TGCTAGCCAC CATGGAGTTG TGGTTAAGCT TGGTCTTCCT  
TGTCTTGTT TTTAAAGGTG TCCAGTGTGA AGTGCAACTG GTGGAGTCTG GGGGAGGCTT  
AGTGCAGCCT GGAGGGTCCC TGCGACTTTC CTGTGCTGCA TCTGGATTCC CGTTCAGTGA  
CTATTACATG TATTGGGTTC GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT

60  
120  
180  
240  
300

B'  
cont.

TAGTCAAGAT	GGTGATATAA	CCGACTATGC	AGACTCCGTA	AAGGGTCGAT	TCACCATCTC	360
CAGAGACAAT	GCAAAGAACA	GCCTGTACCT	GCAATGAAC	AGCCTGAGGG	ACGAGGACAC	420
AGCGTGTAT	TACTGTGCAA	GAGGCCTGGC	GGACGGGGCC	TGGTTTGCTT	ACTGGGGCCA	480
AGGGACTCTG	GTCACGGTCT	CTTCCGCTAG	CACCAAGGGC	CCATCGGTCT	TCCCCCTGGC	540
ACCTCTCTCC	AAGAGCACCT	CTGGGGGCAC	AGCGGCCCTG	GGCTGCCTGG	TCAAGGACTA	600
CTTCCCCGAA	CCGGTGACGG	TGTCGTGGAA	CTCAGGCGCC	CTGACCAGCG	GCGTGACAC	660
CTTCCCGGCT	GTCCTACAGT	CCTCAGGACT	CTACTCCCTC	AGCAGCGTGG	TCACCGTGCC	720
CTCCAGCAGC	TTGGGCACCC	AGACCTACAT	CTGCAACGTG	AATCACAAGC	CCAGCAACAC	780
CAAGGTGGAC	AAGAAAGTTG	GTGAGAGGCC	AGCACAGGGA	GGGAGGGTGT	CTGCTGGGAG	840
CCAGGCTCAG	CGCTCCTGCC	TGGACGCATC	CCGGCTATGC	AGCCCCAGTC	CAGGGCAGCA	900
AGGCAGGCCC	CGTCTGCCTC	TTCACCCGGA	GGCCTCTGCC	CGCCCCACTC	ATGCTCAGGG	960
AGAGGGTCTT	CTGGCTTTTT	CCCAGGCTC	TGGGCAGGCA	CAGGCTAGGT	GGCCCTAACC	1020
CAGGCCCTGC	ACACAAAGGG	GCAGGTGCTG	GGCTCAGACC	TGCCAAGAGC	CATATCCGGG	1080
AGGACCTGTC	CCCTGACCTA	AGCCCCACCC	AAAGGCCAAA	CTCTCCACTC	CCTCAGCTCG	1140
GACACCTTCT	CTCCTCCCAG	ATTCCAGTAA	CTCCCAATCT	TCTCTCTGCA	GAGCCCAAAT	1200
CTTGTTGACAA	AACTCACACA	TGCCCCACCGT	GCCCAGGTAA	GCCAGCCCAG	GCCTCGCCCT	1260
CCAGTCAAG	GCGGGACAGG	TGCCCTAGAG	TAGCCTGCAT	CCAGGGACAG	GGCCAGCCG	1320
GGTGCTGACT	TACCCACCTC	CATCTCTTCC	TCAGCACCTG	AACTCCTGGG	GGGACCGTCA	1380
GTCTTCTCT	TCCCCCAAAA	ACCCAAGGAC	ACCCTCATGA	TCTCCCGGAC	CCCTGAGGTC	1440
ACATGCGTGG	TGGTGACGT	GAGCCACGAA	GACCCTGAGG	TCAAGTTCAA	CTGGTACGTG	1500
GACGGCGTGG	AGGTGCATAA	TGCCAAGACA	AAGCCGCGGG	AGGAGCAGTA	CAACAGCACG	1560
TACCGTGTGG	TCAGCGTCTT	CACCGTCTTG	CACCAGGACT	GGCTGAATGG	CAAGGAGTAC	1620
AAGTGCAAGG	TCTCCAACAA	AGCCCTCCCA	GCCCCATCG	AGAAAACCAT	CTCCAAAGCC	1680
AAAGGTGGGA	CCCGTGGGGT	GCGAGGGCCA	CATGGACAGA	GGCCGGCTCG	GGCCACCCTC	1740
TGCCCTGAGA	GTGACCGCTG	TACCAACCTC	TGTCCCTACA	GGGCAGCCCC	GAGAACCACA	1800
GGTGTTACAC	CTGCCCCCAT	CCCGGGATGA	GCTGACCAAG	AACCAGGTCA	GCCTGACCTG	1860
CCTGGTCAAA	GGCTTCTATC	CCAGCGACAT	CGCCGTGGAG	TGGGAGAGCA	ATGGGCAGCC	1920
GGAGAACAAC	TACAAGACCA	CGCTCCCGT	GCTGGACTCC	GACGGCTCCT	TCTTCCTCTA	1980
CAGCAAGCTC	ACCGTGGACA	AGAGCAGGTG	GCAGCAGGGG	AACGTCTTCT	CATGCTCCGT	2040
GATGCATGAG	GCTCTGCACA	ACCACTACAC	GCAGAAGAGC	CTCTCCCTGT	CTCCGGGTAA	2100
ATGAGTGCAG	CGGCCGGCAA	GCCCCGCTC	CCCGGGCTCT	CGCGGTGCGA	CGAGGATGCT	2160
TGGCAGGTAC	CCCCTGTACA	TACTTCCCGG	GCGCCAGCA	TGGAAATAAA	GCACCCAGCG	2220
CTGCCCTGGG	CCCTGTGCGAG	ACTGTGATGG	TTCTTTCCAC	GGGTGAGGCC	GAGTCTGAGG	2280
CCTGAGTGGC	ATGAGGGAGG	CAGAGCGGGT	CCCACTGTCC	CCACACTGGC	CCAGGCTGTG	2340
CAGGTGTGCC	TGGGCCCCCT	AGGGTGGGGC	TCAGCCAGGG	GCTGCCCTCG	GCAGGGTGGG	2400
GGATTTGCCA	GCGTGGCCCT	CCCTCCAGCA	GCACCTGCCC	TGGGCTGGGC	CACGGGAAGC	2460
CCTAGGAGCC	CTGGGGACA	GACACAGAC	CCCTGCCTCT	GTAGGAGACT	GTCTCTGTTCT	2520
GTGAGCGCCC	CTGTCTCCCT	GACCTCCATG	CCCACTCGGG	GGCATGCCTA	GTCCATGTGC	2580
GTAGGGACAG	GCCTCCCTC	ACCCATCTAC	CCCCACGGCA	CTAACCCTCG	GCTGCCCTGC	2640
CCAGCCTCGC	ACCCGCATGG	GGACACAACC	GACTCCGGGG	ACATGCACTC	TCGGGCCCTG	2700
TGGAGGGACT	GGTGCAGATG	CCCACACACA	CACTCAGCCC	AGACCCGTTC	AACAAACCCC	2760
GCACCTGAGGT	TGGCCGGCCA	CACGGCCACC	ACACACACAC	GTGCACGCC	CACACACGGA	2820
GCCTCACCCG	GGCGAACTGC	ACAGCACCCA	GACCAGAGCA	AGGTCTCTCG	ACACGTGAAC	2880
ACTCTCGGA	CACAGGCCCC	CACGAGCCCC	ACGCGGCACC	TCAAGGCCCA	CGAGCCTCTC	2940
GGCAGCTTCT	CCCATGCTG	ACCTGCTCAG	ACAAACCCAG	CCCTCTCTC	ACAAGGGTGC	3000
CCCTGCAGCC	GCCACACACA	CACAGGGGAT	CACACACCAC	GTACAGTCCC	TGGCCCTGGC	3060
CCACTTCCCA	GTGCCGCCCT	TCCCTGCAGG	ACGGATCAGC	CTCGACTGTG	CCTTCTAGTT	3120
GCCAGCCATC	TGTTGTTTGC	CCCTCCCCCG	TGCCTTCCTT	GACCCTGGAA	GGTGCCACTC	3180
CCACTGTCTT	TTCCTAATAA	AATGAGGAAA	TTGCATCGCA	TTGTCTGAGT	AGGTGTCATT	3240
CTATTCTGGG	GGGTGGGGTG	GGGCAGGACA	GCAAGGGGGA	GGATTGGGAA	GACAATAGCA	3300
GGCATGCTGG	GGATGCGGTG	GGCTCTATGG	CTTCTGAGGC	GGAAAGAACC	AGCTGGGGCT	3360
CTAGGGGGTA	TCCCCACGCG	CCCTGTAGCG	GCGCATTAAG	CGCGGCGGGT	GTGGTGGTTA	3420
CGCGCAGCGT	GACCGCTACA	CTTGCCAGCG	CCCTAGCGCC	CGCTCCTTTC	GCTTTCTTCC	3480
CTTCTTTTCT	CGCCACGTTT	GCCGGGCCTC	TCAAAAAGG	GAAAAAAGC	ATGCATCTCA	3540
ATTAGTCAGC	AACCATAGTC	CCGCCCCATA	CTCCGCCCAT	CCCGCCCCTA	ACTCCGCCCA	3600
GTTCGCCCCA	TTCCTCGCCC	CATGGCTGAC	TAATTTTTTT	TATTTATGCA	GAGGCCGAGG	3660
CCGCCTCGGC	CTCTGAGCTA	TTCCAGAAGT	AGTGAGGAGG	CTTTTTTGGG	GGCCTAGGCT	3720
TTTGCAAAAA	GCTTGACAG	CTCAGGGCTG	CGATTTTCGG	CCAAACTTGA	CGGCAATCCT	3780
AGCGTGAAGG	CTGGTAGGAT	TTTATCCCCG	CTGCCATCAT	GGTTCGACCA	TTGAACTGCA	3840
TCGTGCGCGT	GTCCCAAAAT	ATGGGGATTG	GCAAGAACGG	AGACCTACCC	TGGCCTCCGC	3900

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TCAGGAACGA	GTTCAAGTAC	TTCCAAAGAA	TGACCACAAC	CTCTTCAGTG	GAAGGTAAAC	3960
AGAATCTGGT	GATTATGGGT	AGGAAAACCT	GGTTCTCCAT	TCCTGAGAAG	AATCGACCTT	4020
TAAAGGACAG	AATTAATATA	GTTCTCAGTA	GAGAACTCAA	AGAACCACCA	CGAGGAGCTC	4080
ATTTTCTTGC	CAAAAAGTTTG	GATGATGCCT	TAAGACTTAT	TGAACAACCG	GAATTGGCAA	4140
GTAAAGTAGA	CATGGTTTGG	ATAGTCGGAG	GCAGTTCTGT	TTACCAGGAA	GCCATGAATC	4200
AACCAGGCCA	CCTTAGACTC	TTTGTGACAA	GGATCATGCA	GGAATTTGAA	AGTGACACGT	4260
TTTTCCCAGA	AATTGATTTG	GGGAAATATA	AACTTCTCCC	AGAATACCCA	GGCGTCCTCT	4320
CTGAGGTCCA	GGAGGAAAAA	GGCATCAAGT	ATAAGTTTGA	AGTCTACGAG	AAGAAAAGACT	4380
AACAGGAAGA	TGCTTTCAAG	TTCTCTGCTC	CCCTCCTAAA	GCTATGCATT	TTTATAAGAC	4440
CATGGGACTT	TTGCTGGCTT	TAGATCTCTT	TGTGAAGGAA	CCTTACTTCT	GTGGTGTGAC	4500
ATAATTGGAC	AAACTACCTA	CAGAGATTTA	AAGCTCTAAG	GTAAATATAA	AATTTTTAAG	4560
TGTATAATGT	GTTAAACTAC	TGATTCTAAT	TGTTTGTGTA	TTTTAGATTC	CAACCTATGG	4620
AACTGATGAA	TGGGAGCAGT	GGTGGAATGC	CTTTAATGAG	GAAAACCTGT	TTTGCTCAGA	4680
AGAAATGCCA	TCTAGTGATG	ATGAGGCTAC	TGCTGACTCT	CAACATTCTA	CTCCTCCAAA	4740
AAAGAAGAGA	AAGGTAGAAG	ACCCCAAGGA	CTTTCCTTCA	GAATTGCTAA	GTTTTTTGAG	4800
TCATGCTGTG	TTTAGTAATA	GAACTCTTGC	TTGCTTTGCT	ATTTACACCA	CAAAGGAAAA	4860
AGCTGCACGT	CTATACAAGA	AAATTATTGA	AAAATATTCT	GTAACCTTTA	TAAGTAGGCA	4920
TAACAGTTAT	AATCATAACA	TACTGTTTTT	TCTTACTCCA	CACAGGCATA	GAGTGTCTGC	4980
TATTAATAAC	TATGCTCAAA	AATTGTGTAC	CTTTAGCTTT	TTAATTTGTA	AAGGGGTAA	5040
TAAGGAATAT	TTGATGTATA	GTGCCCTGAC	TAGAGATCAT	AATCAGCCAT	ACCACATTTG	5100
TAGAGGTTTT	ACTTGCTTTA	AAAAACCTCC	CACACCTCCC	CCTGAACCTG	AAACATAAAA	5160
TGAATGCAAT	TGTTGTTGTT	AACTTGTTTA	TTGCAGCTTA	TAATGGTTAC	AAATAAAGCA	5220
ATAGCATCAC	AAATTTACAC	AATAAAGCAT	TTTTTTTACT	GCATTCTAGT	TGTGGTTTGT	5280
CCAAACTCAT	CAATGTATCT	TATCATGTCT	GGATCGGCTG	GATGATCCTC	CAGCGCGGGG	5340
ATCTCATGCT	GGAGTTCTTC	CCCCACCCCA	ACTTGTTTAT	TGCAGCTTAT	AATGGTTACA	5400
AATAAAGCAA	TAGCATCACA	AATTTACAAA	ATAAAGCATT	TTTTTCACTG	CATTCTAGTT	5460
GTGGTTTGTC	CAAACCTATC	AATGTATCTT	ATCATGTCTG	TATACCGTCG	ACCTCTAGCT	5520
AGAGCTTGGC	GTAATCATGG	TCATAGCTGT	TTCTGTGTGT	AAATTGTTAT	CCGCTCACAA	5580
TTCCACACAA	CATACGAGCC	GGAAGCATAA	AGTGTAAGC	CTGGGGTGCC	TAATGAGTGA	5640
GCTAACTCAC	ATTAATTGCG	TTGCGCTCAC	TGCCCGCTTT	CCAGTCGGGA	AACCTGTCGT	5700
GCCAGCTGCA	TTAATGAATC	GGCCAACGCG	CGGGGAGAGG	CGGTTTGCGT	ATTGGGCGCT	5760
CTTCCGCTTC	CTCGCTCACT	GACTCGCTGC	GCTCGGTCGT	TCGGCTGCGG	CGAGCGGTAT	5820
CAGCTCACTC	AAAGGCGGTA	ATACGGTTAT	CCACAGAATC	AGGGGATAAC	GCAGGAAAGA	5880
ACATGTGAGC	AAAAGGCCAG	CAAAAGGCCA	GGAACCGTAA	AAAGGCCGCG	TTGCTGGCGT	5940
TTTTCCATAG	GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA	TCGACGCTCA	AGTCAGAGGT	6000
GGCGAAACCC	GACAGGACTA	TAAAGATACC	AGGCGTTTCC	CCCTGGAAGC	TCCCTCGTGC	6060
GCTCTCCTGT	TCCGACCCTG	CGGCTTACCG	GATACCTGTC	CGCCTTTCTC	CCTTCGGGAA	6120
GCGTGGCGCT	TTCTCAATGC	TCACGCTGTA	GGTATCTCAG	TTCGGTGTAG	GTCGTTGCTG	6180
CCAAGCTGGG	CTGTGTGCAC	GAACCCCCCG	TTCAGCCCGA	CCGCTGCGCC	TTATCCGGTA	6240
ACTATCGTCT	TGAGTCCAAC	CCGGTAAGAC	ACGACTTATC	GCCACTGGCA	GCAGCCACTG	6300
GTAACAGGAT	TAGCAGAGCG	AGGTATGTAG	GCGGTGCTAC	AGAGTTCTTG	AAGTGGTGGC	6360
CTAACTACGG	CTACACTAGA	AGGACAGTAT	TTGGTATCTG	CGCTCTGCTG	AAGCCAGTTA	6420
CCTTCGGAAA	AAGAGTTGGT	AGCTCTTGAT	CCGGCAAACA	AACCACCGCT	GGTAGCGGTG	6480
GTTTTTTTGT	TTGCAAGCAG	CAGATTACGC	GCAGAAAAAA	AGGATCTCAA	GAAGATCCTT	6540
TGATCTTTTC	TACGGGGTCT	GACGCTCAGT	GGAACGAAAA	CTCACGTTAA	GGGATTTTGG	6600
TCATGAGATT	ATCAAAAAGG	ATCTTCACCT	AGATCCTTTT	AAATTAAAAA	TGAAGTTTAA	6660
AATCAATCTA	AAGTATATAT	GAGTAAACTT	GGTCTGACAG	TTACCAATGC	TTAATCAGTG	6720
AGGCACCTAT	CTCAGCGATC	TGTCTATTTT	GTTTCATCCAT	AGTTGCCTGA	CTCCCCGTCG	6780
TGTAGATAAC	TACGATACGG	GAGGGCTTAC	CATCTGGCCC	CAGTGCTGCA	ATGATACCGC	6840
GAGACCCACG	CTCACC GGCT	CCAGATTTAT	CAGCAATAAA	CCAGCCAGCC	GGAAGGGCCG	6900
AGCGCAGAAG	TGGTCCTGCA	ACTTTATCCG	CCTCCATCCA	GTCTATTAAAT	TGTTGCCGGG	6960
AAGCTAGAGT	AAGTAGTTTG	CCAGTTAATA	GTTTGCGCAA	CGTTGTTGCC	ATTGCTACAG	7020
GCATCGTGGT	GTCACGCTCG	TCGTTTGGTA	TGGCTTCATT	CAGCTCCGGT	TCCCAACGAT	7080
CAAGGCGAGT	TACATGATCC	CCCATGTTGT	GCAAAAAAGC	GGTTAGCTCC	TTCGGTCTCT	7140
CGATCGTTGT	CAGAAGTAAG	TTGGCCGCGAG	TGTTATCACT	CATGGTTATG	GCAGCACTGC	7200
ATAATTCTCT	TACTGTCATG	CCATCCGTAA	GATGCTTTTC	TGTGACTGGT	GAGTACTCAA	7260
CCAAGTCATT	CTGAGAATAG	TGTATGCGGC	GACCGAGTTG	CTCTTGCCCG	GCGTCAATAC	7320
GGGATAATAC	CGCGCCACAT	AGCAGAACTT	TAAAAGTGCT	CATCATTTGA	AAACGTTCTT	7380
CGGGGCGAAA	ACTCTCAAGG	ATCTTACCGC	TGTTGAGATC	CAGTTCGATG	TAACCCACTC	7440
GTGCACCCAA	CTGATCTTCA	GCATCTTTTA	CTTTCACCAG	CGTTTCTGGG	TGAGCAAAAA	7500

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CAGGAAGGCA	AAATGCCGCA	AAAAAGGGAA	TAAGGGCGAC	ACGGAAATGT	TGAATACTCA	7560
TACTCTTCCT	TTTTCAATAT	TATTGAAGCA	TTTATCAGGG	TTATTGTCTC	ATGAGCGGAT	7620
ACATATTTGA	ATGTATTTAG	AAAAATAAAC	AAATAGGGGT	TCCGCGCACA	TTTCCCCGAA	7680
AAGTGCCACC	TGACGTGCAC	GGATCGGGAG	ATCTGCTAGG	TGACCTGAGG	CGCGCCGGCT	7740
TCGAATAGCC	AGAGTAACCT	TTTTTTTTTA	TTTTATTTTA	TTTTATTTT	GAGATGGAGT	7800
TTGGCGCCGA	TCTCCCGATC	CCCTATGGTC	GACTCTCAGT	ACAATCTGCT	CTGATGCCGC	7860
ATAGTTAAGC	CAGTATCTGC	TCCCTGCTTG	TGTGTTGGAG	GTCGCTGAGT	AGTGCGCGAG	7920
CAAAATTTAA	GCTACAACAA	GGCAAGGCTT	GACCGACAAT	TGCATGAAGA	ATCTGCTTAG	7980
GGTTAGGCGT	TTTGCCTGTC	TTCGCGATGT	ACGGGCCAGA	TATACGCGTT	GACATTGATT	8040
ATTGACTAGT	TATTAATAGT	AATCAATTAC	GGGGTCATTA	GTTTCATAGC	CATATATGGA	8100
GTTCCGCGTT	ACATAACTTA	CGGTAAATGG	CCCGCCTGGC	TGACCGCCCA	ACGACCCCCG	8160
CCCATTGACG	TCAATAATGA	CGTATGTTCC	CATAGTAACG	CCAATAGGGA	CTTTCCATTG	8220
ACGTCAATGG	GTGGACTATT	TACGGTAAAC	TGCCCCACTG	GCAGTACATC	AAGTGTATCA	8280
TATGCCAAGT	ACGCCCCCTA	TTGACGTCAA	TGACGGTAAA	TGGCCCCGCT	GGCATTATGC	8340
CCAGTACATG	ACCTTATGGG	ACTTTCCTAC	TTGGCAGTAC	ATCTACGTAT	TAGTCATCGC	8400
TATTACCATG	GTGATGCGGT	TTTGGCAGTA	CATCAATGGG	CGTGGATAGC	GGTTTGACTC	8460
ACGGGGGATT	CCAAGTCTCC	ACCCCATTTA	CGTCAATGGG	AGTTTGTTTT	GGCACCAGAA	8520
TCAACGGGGA	TTTCCAAAAT	GTCGTAACAA	CTCCGCCCCA	TTGACGCAAA	TGGGCGGTAG	8580
GCGTGACGG	TGGGAGGTCT	ATATAAGCAG	AGCTCTCTGG	CTAACTAGAG	AACCCACTGC	8640
TTACTGGCTT	ATCGAAATTA	ATACGACTCA	CTATAGGGAG	ACCCAAGCTT		8690

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7874 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGTACCAATT	TAAATTGATA	TCTCCTTAGG	TCTCGAGTCT	CTAGATAACC	GGTCAATCGA	60
TTGGAATTCT	TGCGGCCGCT	TGCTAGCACC	AAGGGCCCAT	CGGTCTTCCC	CCTGGCACCC	120
TCCTCCAAGA	GCACCTCTGG	GGGCACAGCG	GCCCTGGGCT	GCCTGGTCAA	GGACTACTTC	180
CCCGAACCAG	TGACGGTGTC	GTGGAATCTA	GGCGCCCTGA	CCAGCGCGCT	GCACACCTTC	240
CCGCTGTCC	TACAGTCCTC	AGGACTCTAC	TCCCTCAGCA	GCGTGGTCAC	CGTGCCCTCC	300
AGCAGCTTGG	GCACCCAGAC	CTACATCTGC	AACGTGAATC	ACAAGCCCAG	CAACACCAAG	360
GTGGACAAGA	AAGTTGGTGA	GAGGCCAGCA	CAGGGAGGGA	GGGTGTCTGC	TGGAAGCCAG	420
GCTCAGCGCT	CCTGCCTGGA	CGCATCCCAG	CTATGCAGCC	CCAGTCCAGG	GCAGCAAGGC	480
AGGCCCCGTC	TGCTCTTCA	CCCGGAGGCC	TCTGCCCGCC	CCACTCATGC	TCAGGGAGAG	540
GGTCTTCTGG	CTTTTCCCC	AGGCTCTGGG	CAGGCACAGG	CTAGGTGCCC	CTAACCCAGG	600
CCCTGCACAC	AAAGGGGCAG	GTGCTGGGCT	CAGACCTGCC	AAGAGCCATA	TCCGGGAGGA	660
CCCTGCCCCCT	GACCTAAGCC	CACCCCAAAG	GCCAACTCT	CCACTCCCTC	AGCTCGGACA	720
CCTTCTCTCC	TCCAGATTCC	CAGTAACTCC	CAATCTTCTC	TCTGCAGAGC	CCAAATCTTG	780
TGACAAAAC	CACACATGCC	CACCGTGCCC	AGGTAAGCCA	GCCAGGCCT	CGCCCTCCAG	840
CTCAAGGCGG	GACAGGTGCC	CTAGAGTAGC	CTGCATCCAG	GGACAGGCC	CAGCCGGGTG	900
CTGACACGTC	CACCTCCATC	TCTTCCTCAG	CACCTGAACT	CCTGGGGGGA	CCGTCAGTCT	960
TCCTCTTCCC	CCCAAAACCC	AAGGACACCC	TCATGATCTC	CCGGACCCCT	GAGGTCACAT	1020
GCGTGGTGGT	GGACGTGAGC	CACGAAGACC	CTGAGGTCAA	GTTCAACTGG	TACGTGGACG	1080
GCGTGGAGGT	GCATAATGCC	AAGACAAAGC	CGCGGGAGGA	GCAGTACAAC	AGCACGTACC	1140
GTGTGGTCAG	CGTCTCACC	GTCCTGCACC	AGGACTGGCT	GAATGGCAAG	GAGTACAAGT	1200
GCAAGGTCTC	CAACAAAGCC	CTCCCAGCCC	CCATCGAGAA	AACCATCTCC	AAAGCCAAAG	1260
GTGGGACCCG	TGGGGTGCGA	GGGCCACATG	GACAGAGGCC	GGCTCGGCCC	ACCCTCTGCC	1320
CTGAGAGTGA	CCGTGTACC	AACCTGTGTC	CTACAGGGC	AGCCCCGAGA	ACCACAGGTG	1380
TACACCTGTC	CCCCATCCCG	GGATGAGCTG	ACCAAGAACC	AGGTCAGCCT	GACCTGCCTG	1440
GTCAAAGGCT	TCTATCCAG	CGACATCGCC	GTGGAGTGGG	AGAGCAATGG	GCAGCCGGAG	1500
AACAACACTA	AGACCACGCC	TCCCGTGCTG	GACTCCGACG	GCTCCTTCTT	CCTCTACAGC	1560
AAGCTCACCG	TGGACAAGAG	CAGGTGGCAG	CAGGGGAACG	TCTTCTCATG	CTCCGTGATG	1620

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CATGAGGCTC	TGCACAACCA	CTACACGCAG	AAGAGCCTCT	CCCTGTCTCC	GGGTAAATGA	1680
GTGCGACGGC	CGGCAAGCCC	CCGCTCCCCG	GGCTCTCGCG	GTGCGACGAG	GATGCTTGGC	1740
ACGTACCCCC	TGTACATACT	TCCCGGGCGC	CCAGCATGGA	AATAAAGCAC	CCAGCGCTGC	1800
CCTGGGCCCC	TGCAGAGACTG	TGATGGTTCT	TTCCACGGGT	CAGGCCGAGT	CTGAGGCCTG	1860
AGTGGCATGA	GGGAGGCAGA	GCGGGTCCCA	CTGTCCCCAC	ACTGGCCCAG	GCTGTGCAGG	1920
TGTGCCTGGG	CCCCCTAGGG	TGGGGCTCAG	CCAGGGGCTG	CCCTCGGCAG	GGTGGGGGAT	1980
TTGCCAGCGT	GGCCCTCCCT	CCAGCAGCAC	CTGCCCTGGG	CTGGGCCACG	GGAAGCCCTA	2040
GGAGCCCCCTG	GGGACAGACA	CACAGCCCCCT	GCCTCTGTAG	GAGACTGTCC	TGTTCTGTGA	2100
GCGCCCCCTGT	CCTCCCGACC	TCCATGCCCA	CTCGGGGGCA	TGCTGGGGAT	GCGGTGGGCT	2160
CTATGGCTTC	TGAGGCGGAA	AGAACCAGCT	GGGGCTCTAG	GGGGTATCCC	CACGCGCCCT	2220
GTAGCGGCGC	ATTAAGCGCG	GCGGGTGTGG	TGGTTACGCG	CAGCGTGACC	GCTACACTTG	2280
CCAGCGCCCT	AGCGCCCGCT	CCTTTCGCTT	TCTTCCCTTC	CTTCTCGCC	ACGTTCCGCC	2340
GCTTTCCTCG	TCAAGCTCTA	AATCGGGGCA	TCCCTTTAGG	GTTCCGATT	AGTGCTTTAC	2400
GGCACCTCGA	CCCCAAAAA	CTTGATTAGG	GTGATGGTTC	ACGTAGTGGG	CCATCGCCCT	2460
GATAGACGGT	TTTTCGCCCT	TTGACGTTGG	AGTCCACGTT	CTTTAATAGT	GGACTCTTGT	2520
TCCAAACTGG	AACAACACTC	AACCCTATCT	CGGTCTATTC	TTTTGATTTA	TAAGGGATTT	2580
TGGGGATTTC	GGCCTATTGG	TTAAAAATG	AGCTGATTTA	ACAAAAATT	AACGCGAATT	2640
AATTCTGTGG	AATGTGTGTC	AGTTAGGGTG	TGGAAAGTCC	CCAGGCTCCC	CAGGCAGGCA	2700
GAAGTATGCA	AAGCATGCAT	CTCAATTAGT	CAGCAACCAT	AGTCCCGCCC	CTAACTCCGC	2760
CCATCCCGCC	CCTAACTCCG	CCCAGTTCGG	CCCATTCTCC	GCCCCATGGC	TGACTAATTT	2820
TTTTTATTTA	TGCAGAGGCC	GAGGCCGCCT	CGGCCTCTGA	GCTATTCCAG	AAGTAGTGAG	2880
GAGGCTTTTT	TGGAGGCCTA	GGCTTTTGCA	AAAAGCTTGG	ACAGCTCAGG	GCTGCGATTT	2940
CGCGCCAAAC	TTGACGGCAA	TCCTAGCGTG	AAGGCTGGTA	GGATTTTATC	CCCGCTGCCA	3000
TCATGGTTTCG	ACCATTGAAC	TGCATCGTCG	CCGTGTCCCA	AAATATGGGG	ATTGGCAAGA	3060
ACGGAGACCT	ACCCTGGCCT	CCGCTCAGGA	ACGAGTTCAA	GTACTTCCAA	AGAATGACCA	3120
CAACCTCTTC	AGTGGAAGGT	AAACAGAATC	TGGTGATTAT	GGGTAGGAAA	ACCTGGTTCT	3180
CCATTCCCTGA	GAAGAATCGA	CCTTTAAAGG	ACAGAATTAA	TATAGTTCTC	AGTAGAGAAC	3240
TCAAAGAACC	ACCACGAGGA	GCTCATTTTC	TTGCCAAAAG	TTTGATGAT	GCCTTAAGAC	3300
TTATTGAACA	ACCGGAATTG	GCAAGTAAAG	TAGACATGGT	TTGGATAGTC	GGAGGCAGTT	3360
CTGTTTACCA	GGAAGCCATG	AATCAACCAG	GCCACCTTAG	ACTCTTTGTG	ACAAGGATCA	3420
TGCAGGAATT	TGAAAGTGAC	ACGTTTTTCC	CAGAAATTGA	TTTGGGAAA	TATAAACTTC	3480
TCCCAGAATA	CCCAGGCGTC	CTCTCTGAGG	TCCAGGAGGA	AAAAGGCATC	AAGTATAAGT	3540
TTGAAGTCTA	CGAGAAGAAA	GACTAACAGG	AAGATGCTTT	CAAGTTCTCT	GCTCCCTCC	3600
TAAAGCTATG	CATTTTATA	AGACCATGGG	ACTTTTGCTG	GCTTTAGATC	TCTTTGTGAA	3660
GGAACCTTAC	TTCTGTGGTG	TGACATAATT	GGACAACTA	CCTACAGAGA	TTTAAAGCTC	3720
TAAGGTAAAT	ATAAAATTTT	TAAGTGATATA	ATGTGTTAAA	CTACTGATTC	TAATTGTTTG	3780
TGTATTTTAG	ATTTCAACCT	ATGGAATGCA	TGAATGGGAG	CAGTGGTGGA	ATGCCCTTAA	3840
TGAGGAAAAC	CTGTTTTGCT	CAGAAGAAAT	GCCATCTAGT	GATGATGAGG	CTACTGCTGA	3900
CTCTCAACAT	TCTACTCCTC	CAAAAAAGAA	GAGAAAGGTA	GAAGACCCCA	AGGACTTTCC	3960
TTCAGAATTG	CTAAGTTTTT	TGAGTCATGC	TGTGTTTAGT	AATAGAACTC	TTGCTTGCTT	4020
TGCTATTTAC	ACCACAAAGG	AAAAAGCTGC	ACTGCTATAC	AAGAAAATTA	TGGAAAAATA	4080
TTCTGTAAAC	TTTATAAGTA	GGCATAACAG	TTATAATCAT	AACATACTGT	TTTTTCTTAC	4140
TCCACACAGG	CATAGAGTGT	CTGCTATTAA	TAAGTATGCT	CAAAAATTGT	GTACCTTTAG	4200
CTTTTAAATT	TGTAAAGGGG	TTAATAAGGA	ATATTTGATG	TATAGTGCCT	TGACTAGAGA	4260
TCATAATCAG	CCATACCACA	TTGTAGAGG	TTTACTTGC	TTTAAAAAAC	CTCCCACACC	4320
TCCCCTGAA	CCTGAAACAT	AAAATGAATG	CAATTGTTGT	TGTTAACTTG	TTTATTGCAG	4380
CTTATAATGG	TTACAAATAA	AGCAATAGCA	TCACAAATTT	CACAAATAAA	GCATTTTTTT	4440
CACTGCATTTC	TAGTTGTGGT	TTGTCCAAAC	TCATCAATGT	ATCTTATCAT	GTCTGGATCG	4500
GCTGGATGAT	CCTCCAGCGC	GGGGATCTCA	TGCTGGAGTT	CTTCGCCCCAC	CCCAACTTGT	4560
TTATTGCAGC	TTATAATGGT	TACAAATAAA	GCAATAGCAT	CACAAATTTT	ACAAATAAAG	4620
CATTTTTTTT	ACTGCATTCT	AGTTGTGGTT	TGTCCAAACT	CATCAATGTA	TCTTATCATG	4680
TCTGTATACC	GTCGACCTCT	AGCTAGAGCT	TGGCGTAATC	ATGGTCATAG	CTGTTTCTCTG	4740
TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	ACAACATACG	AGCCGGAAGC	ATAAAGTGTA	4800
AAGCCTGGGG	TGCCTAATGA	GTGAGCTAAC	TCACATTAAAT	TGCGTTGCGC	TCCTGCCCCG	4860
CTTTCCAGTG	GGGAAACCTG	TCGTGCCAGC	TGCATTAAATG	AATCGGCCAA	CGCGCGGGGA	4920
GAGGCGGTTT	GCGTATTGGG	CGCTCTTCCG	CTTCTCGCT	CCTGACTCG	CTGCGCTCGG	4980
TCGTTCGGCT	GCGGCGAGCG	GTATCAGCTC	ACTCAAAGGC	GGTAATACGG	TTATCCACAG	5040
AATCAGGGGA	TAACGCAGGA	AAGAACATGT	GAGCAAAAGG	CCAGCAAAAG	GCCAGGAACC	5100
GTAATAAGGC	CGCGTTGCTG	GCGTTTTTCC	ATAGGCTCCG	CCCCCTGAC	GAGCATCACA	5160
AAAATCGACG	CTCAAGTCAG	AGGTGGCGAA	ACCCGACAGG	ACTATAAAGA	TACCAGGCGT	5220

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TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATAACC 5280  
 TGTCGCCTTT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA ATGCTCACGC TGTAGGTATC 5340  
 TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTTACG 5400  
 CCGACCGCTG CGCCTTATCC GGTAACATATC GTCTTGAGTC CAACCCGGTA AGACACGACT 5460  
 TATCGCCACT GGCAGCAGCC ACTGGTAACA GGATTAGCAG AGCGAGGTAT GTAGGCGGTG 5520  
 CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA GTATTTGGTA 5580  
 TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGCA 5640  
 AACAAACCAC CGCTGGTAGC GGTGGTTTTT TTGTTTGCAA GCAGCAGATT ACGCGCAGAA 5700  
 AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT CAGTGGAACG 5760  
 AAACTCACG TTAAGGGATT TTGGTCATGA GATTATCAAA AAGGATCTTC ACCTAGATCC 5820  
 TTTTAAATTA AAAATGAAGT TTTAAATCAA TCTAAAGTAT ATATGAGTAA ACTTGGTCTG 5880  
 ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCTCAGC GATCTGTCTA TTTCGTTTCA 5940  
 CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG 6000  
 GCCCCAGTGC TGCAATGATA CCGCGAGACC CACGCTCACC GGCTCCAGAT TTATCAGCAA 6060  
 TAAACCAGCC AGCCGGAAGG GCCGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCCTCCA 6120  
 TCCAGTCTAT TAATTGTTGC CGGGAAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTTGC 6180  
 GCAACGTTGT TGCCATTGCT ACAGGCATCG TGGTGTACG CTCGTCGTTT GGTATGGCTT 6240  
 CATTGAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA 6300  
 AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG TAAGTTGGCC GCAGTGTAT 6360  
 CACTCATGGT TATGGCAGCA CTGCATAATT CTCTTACTGT CATGCCATCC GTAAGATGCT 6420  
 TTTCTGTGAC TGGTGAGTAC TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACCGA 6480  
 GTTGCTCTTG CCCGGCGTCA ATACGGGATA ATACCGCGCC ACATAGCAGA ACTTTAAAAG 6540  
 TGCTCATCAT TGGAAAACGT TCTTCGGGGC GAAAACTCTC AAGGATCTTA CCGCTGTTGA 6600  
 GATCCAGTTC GATGTAACCC ACTCGTGAC CCAACTGATC TTCAGCATCT TTTACTTTCA 6660  
 CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG GGAATAAGGG 6720  
 CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTTCA ATATTATTGA AGCATTATC 6780  
 AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG 6840  
 GGGTTCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT CGACGGATCG GGAGATCTGC 6900  
 TAGGTGACCT GAGGCGCGCC GGCTTCGAAT AGCCAGAGTA ACCTTTTTTT TTAATTTTAT 6960  
 TTTATTTTAT TTTTGAGATG GAGTTTGGCG CCGATCTCCC GATCCCCTAT GGTCGACTCT 7020  
 CAGTACAATC TGCTCTGATG CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT 7080  
 GGAGGTGCT GAGTAGTGCG CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA 7140  
 CAATTGCATG AAGAATCTGC TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG ATGTACGGGC 7200  
 CAGATATACG CGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC 7260  
 ATTAGTTCAT AGCCCATATA TGGAGTTCGG CGTTACATAA CTTACGGTAA ATGGCCCGCC 7320  
 TGGCTGACCG CCCAACGACC CCCGCCATT GACGTCAATA ATGACGTATG TTCCCATAGT 7380  
 AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAC TATTTACGGT AAACGCCCCA 7440  
 CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG 7500  
 TAAATGGCCC GCCTGGCATT ATGCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA 7560  
 GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA 7620  
 TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA 7680  
 TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC 7740  
 CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT 7800  
 CTGGCTAACT AGAGAACCCA CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG 7860  
 GGAGACCCAA GCTT 7874

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Asp Tyr

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Tyr Ile Ser Gln Asp Gly Asp Ile Thr Asp Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Gly Leu Ala Asp Gly Ala Trp Phe Ala Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 1 5 10 15  
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80  
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95  
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 100 105 110  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
 115 120 125  
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 130 135 140  
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
 145 150 155 160  
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 165 170 175  
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
 180 185 190  
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Asp Lys Val Ser Asn  
 195 200 205  
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
 210 215 220  
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
 225 230 235 240  
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
 245 250 255  
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 260 265 270

B' ant.



Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 275 280 285  
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
 290 295 300  
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
 305 310 315 320  
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 325 330

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 1 5 10 15  
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80  
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95  
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 100 105 110  
 Pro Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 115 120 125  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 130 135 140  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 145 150 155 160  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 165 170 175  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 180 185 190  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 195 200 205  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 210 215 220

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

B' cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu Val Asn Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Lys Val Ser Cys Val Thr Ser Gly Phe Thr Phe Ser Asp Tyr  
20 25 30  
Tyr Met Tyr Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val  
35 40 45  
Ala Tyr Ile Ser Gln Gly Gly Asp Ile Thr Asp Tyr Pro Asp Thr Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Ser Arg Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys  
85 90 95  
Ala Arg Gly Leu Asp Asp Gly Ala Trp Phe Ala Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Val Ala Ser Thr Lys Gly Pro Ser Val Phe  
115 120 125  
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
130 135 140  
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
145 150 155 160  
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
165 170 175  
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
180 185 190  
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
195 200 205  
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys  
210 215 220  
Thr His Thr Cys Pro Pro Cys Pro Gly Gln Pro Arg Glu Pro Gln Val  
225 230 235 240  
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
245 250 255  
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
260 265 270  
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
275 280 285  
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
290 295 300  
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
305 310 315 320  
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
325 330 335  
Pro Gly Lys

B'  
wref.